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(54) Title: MBCATS AS MODIFIERS OF THE BETA-CATENIN PATHWAY AND METHODS OF USE

(57) Abstract: Human MBCAT genes are identified as modulators of the beta-catenin pathway, and thus are therapeutic targets for disorders associated with defective beta-catenin function. Methods for identifying modulators of beta-catenin, comprising screening for agents that modulate the activity of MBCAT are provided.

MBCATs AS MODIFIERS OF THE BETA-CATENIN PATHWAY AND METHODS OF USE

REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. provisional patent applications 60/340,213 filed 12/13/2001, 60/340,314, filed 12/13/2001, 60/340,322 filed 12/13/2001, and 60/357,502 filed 2/15/2002. The contents of the prior applications are hereby incorporated in their entirety.

BACKGROUND OF THE INVENTION

Beta-catenin is an adherens junction protein. Adherens junctions (AJs; also called the zonula adherens) are critical for the establishment and maintenance of epithelial layers, such as those lining organ surfaces. AJs mediate adhesion between cells, communicate a signal that neighboring cells are present, and anchor the actin cytoskeleton. In serving these roles, AJs regulate normal cell growth and behavior. At several stages of embryogenesis, wound healing, and tumor cell metastasis, cells form and leave epithelia. This process, which involves the disruption and reestablishment of epithelial cell-cell contacts, may be regulated by the disassembly and assembly of AJs. AJs may also function in the transmission of the 'contact inhibition' signal, which instructs cells to stop dividing once an epithelial sheet is complete.

The AJ is a multiprotein complex assembled around calcium-regulated cell adhesion molecules called cadherins (Peifer, M.(1993) Science 262: 1667-1668). Cadherins are transmembrane proteins: the extracellular domain mediates homotypic adhesion with cadherins on neighboring cells, and the intracellular domain interacts with cytoplasmic proteins that transmit the adhesion signal and anchor the AJ to the actin cytoskeleton. These cytoplasmic proteins include the alpha-, beta-, and gamma-catenins. The beta-catenin protein shares 70% amino acid identity with both plakoglobin, which is found in desmosomes (another type of intracellular junction), and the product of the Drosophila segment polarity gene 'armadillo'. Armadillo is part of a multiprotein AJ complex in Drosophila that also includes some homologs of alpha-catenin and cadherin, and genetic studies indicate that it is required for cell adhesion and cytoskeletal integrity.

Beta-catenin, in addition to its role as a cell adhesion component, also functions as a transcriptional co-activator in the Wnt signaling pathway through its interactions with

the family of Tcf and Lef transcription factors (for a review see Polakis, (1999) Current Opinion in Genetics & Development, 9:15–21 and Gat U., et al., (1998) Cell 95:605-614).

The APC gene, which is mutant in adenomatous polyposis of the colon, is a negative regulator of beta-catenin signaling (Korinek, V. et al., (1997) Science 275: 1784-1787; Morin, P. J., et al., (1997) Science 275: 1787-1790). The APC protein normally binds to beta-catenin and, in combination with other proteins (including glycogen synthase kinase-3b and axin, is required for the efficient degradation of b-catenin. The regulation of beta-catenin is critical to the tumor suppressive effect of APC and that this regulation can be circumvented by mutations in either APC or beta-catenin.

While mammals contain only a single beta-catenin gene, *C. elegans* contains three (Korswagen HC, et al., (2000) Nature 406:527-32). Each worm beta-catenin appears to carry out unique functions (Korswagen HC, et al., (2000) Nature 406:527-32, Nartarajan L et al. (2001) Genetics 159: 159-72). Because of the divergence of function in *C. elegans*, it is possible to specifically study beta-catenin role in cell adhesion, which is mediated by the *C. elegans* beta-catenin HMP-2.

The Drosophila 'discs large' tumor suppressor protein, Dlg, is the prototype of a family of proteins termed MAGUKs (membrane-associated guanylate kinase homologs). MAGUKs are localized at the membrane-cytoskeleton interface, usually at cell-cell junctions, where they appear to have both structural and signaling roles. They contain several distinct domains, including a modified guanylate kinase domain, an SH3 motif, and 1 or 3 copies of the DHR (GLGF/PDZ) domain. Recessive lethal mutations in the 'discs large' tumor suppressor gene interfere with the formation of septate junctions (thought to be the arthropod equivalent of tight junctions) between epithelial cells, and they also cause neoplastic overgrowth of imaginal discs, suggesting a role for cell junctions in proliferation control. A homolog of the Drosophila Dlg protein was isolated from human B lymphocytes (Lue et al., (1994) Proc. Nat. Acad. Sci. 91: 9818-9822) and shown to bind directly to the membrane cytoskeletal protein 4.1. The presence of human DLG isoforms with or without the protein 4.1 binding domain suggested that the tissue-specific cytoskeletal interactions of the protein may be regulated by alternative splicing of its transcripts.

DLG1 may function as a coupler of tyrosine kinase and a voltage-gated potassium channel in T lymphocytes (Hanada, T., et al., (1997) J. Biol. Chem. 272: 26899-26904). In Drosophila, lethal giant larvae (Lgl) is essential for asymmetric cortical localization of all basal determinants in mitotic neuroblasts, and is therefore indispensable for neural fate

decisions (Ohshiro, T., et al., (2000) Nature 408: 593-596). Lgl, which itself is uniformly cortical, interacts with several types of myosin to localize the determinants. Dlg, another tumor suppressor gene, participates in this process by regulating the localization of Lgl. The localization of the apical components is unaffected in Lgl or Dlg mutants. Thus, Lgl and Dlg act in a common process that differentially mediates cortical protein targeting in mitotic neuroblasts, and creates intrinsic differences between daughter cells.

DLG2, DLG3, and DLG4 are also members of the MAGUK family.

DLG2 (chapsyn-110) and DLG4 (PSD95) each mediate the clustering of NMDA receptors and potassium channels. The proper distribution of voltage-gated and ligand-gated ion channels on the neuronal surface is critical for the processing and transmission of electrical signals in neurons. Chapsyn-110 and PSD95 heteromultimerize with each other and are recruited into the same NMDA receptor and potassium channel clusters. These 2 MAGUK proteins may interact at postsynaptic sites to form a multimeric scaffold for the clustering of receptors, ion channels, and associated signaling proteins (Kim, E., et al., (1996) Neuron 17: 103-113).

DLG3 interacts with the C-terminal region of the APC tumor suppressor protein, and may negatively regulate cell proliferation through its interaction with the APC protein (Makino, K., et al., (1997) Oncogene 14: 2425-2433).

Organ specific differentiation is effected through cell-cell interactions. Mesenchymal stromal cells act to direct growth and differentiation of epithelial cells. Such stromal-epithelial interactions lead to complete organogenesis and maintenance of homeostasis in adult tissues. In cancer, carcinoma epithelial cells induce a reactive stroma. Reactive stroma differentially influences rate of tumorigenesis through unknown mechanisms. Defining specific mechanisms of reciprocal stromal-epithelial signaling and genes and proteins involved in the system, phenotypic switching of stroma, and the role of reactive stroma in cancer progression is therefore highly desired.

The ability to manipulate the genomes of model organisms such as *C. elegans* provides a powerful means to analyze biochemical processes that, due to significant evolutionary conservation, have direct relevance to more complex vertebrate organisms. Due to a high level of gene and pathway conservation, the strong similarity of cellular processes, and the functional conservation of genes between these model organisms and mammals, identification of the involvement of novel genes in particular pathways and their functions in such model organisms can directly contribute to the understanding of the correlative pathways and methods of modulating them in mammals (see, for example,

Dulubova I, et al, J Neurochem 2001 Apr;77(1):229-38; Cai T, et al., Diabetologia 2001 Jan;44(1):81-8; Pasquinelli AE, et al., Nature. 2000 Nov 2;408(6808):37-8; Ivanov IP, et al., EMBO J 2000 Apr 17;19(8):1907-17; Vajo Z et al., Mamm Genome 1999 Oct;10(10):1000-4). For example, a genetic screen can be carried out in an invertebrate model organism having underexpression (e.g. knockout) or overexpression of a gene (referred to as a "genetic entry point") that yields a visible phenotype. Additional genes are mutated in a random or targeted manner. When a gene mutation changes the original phenotype caused by the mutation in the genetic entry point, the gene is identified as a "modifier" involved in the same or overlapping pathway as the genetic entry point. When the genetic entry point is an ortholog of a human gene implicated in a disease pathway, such as beta-catenin, modifier genes can be identified that may be attractive candidate targets for novel therapeutics.

All references cited herein, including patents, patent applications, publications, and sequence information in referenced Genbank identifier numbers, are incorporated herein in their entireties.

SUMMARY OF THE INVENTION

We have discovered genes that modify the beta-catenin pathway in *C. elegans*, and identified their human orthologs, hereinafter referred to as modifiers of beta-catenin (MBCAT). The invention provides methods for utilizing these beta-catenin modifier genes and polypeptides to identify MBCAT-modulating agents that are candidate therapeutic agents that can be used in the treatment of disorders associated with defective or impaired beta-catenin function and/or MBCAT function. Preferred MBCAT-modulating agents specifically bind to MBCAT polypeptides and restore beta-catenin function. Other preferred MBCAT-modulating agents are nucleic acid modulators such as antisense oligomers and RNAi that repress MBCAT gene expression or product activity by, for example, binding to and inhibiting the respective nucleic acid (i.e. DNA or mRNA).

MBCAT modulating agents may be evaluated by any convenient *in vitro* or *in vivo* assay for molecular interaction with an MBCAT polypeptide or nucleic acid. In one embodiment, candidate MBCAT modulating agents are tested with an assay system comprising a MBCAT polypeptide or nucleic acid. Agents that produce a change in the activity of the assay system relative to controls are identified as candidate beta-catenin modulating agents. The assay system may be cell-based or cell-free. MBCAT-

modulating agents include MBCAT related proteins (e.g. dominant negative mutants, and biotherapeutics); MBCAT-specific antibodies; MBCAT-specific antisense oligomers and other nucleic acid modulators; and chemical agents that specifically bind to or interact with MBCAT or compete with MBCAT binding partner (e.g. by binding to an MBCAT binding partner). In one specific embodiment, a small molecule modulator is identified using a binding assay. In specific embodiments, the screening assay system is selected from an apoptosis assay, a cell proliferation assay, an angiogenesis assay, and a hypoxic induction assay.

In another embodiment, candidate beta-catenin pathway modulating agents are further tested using a second assay system that detects changes in the beta-catenin pathway, such as angiogenic, apoptotic, or cell proliferation changes produced by the originally identified candidate agent or an agent derived from the original agent. The second assay system may use cultured cells or non-human animals. In specific embodiments, the secondary assay system uses non-human animals, including animals predetermined to have a disease or disorder implicating the beta-catenin pathway, such as an angiogenic, apoptotic, or cell proliferation disorder (e.g. cancer).

The invention further provides methods for modulating the MBCAT function and/or the beta-catenin pathway in a mammalian cell by contacting the mammalian cell with an agent that specifically binds a MBCAT polypeptide or nucleic acid. The agent may be a small molecule modulator, a nucleic acid modulator, or an antibody and may be administered to a mammalian animal predetermined to have a pathology associated the beta-catenin pathway.

DETAILED DESCRIPTION OF THE INVENTION

Genetic screens were designed to identify modifiers of the beta-catenin pathway in *C. elegans*. A weak allele of beta-catenin was used in our screen (a homozygous viable mutant of beta-catenin, allele qm39). The hmp-2 (qm-39) strain produces larval worms with a highly penetrant lumpy body phenotype in first stage larval worms (L1s). Various specific genes were silenced by RNA inhibition (RNAi). Methods for using RNAi to silence genes in *C. elegans* are known in the art (Fire A, et al., 1998 Nature 391:806-811; Fire, A. Trends Genet. 15, 358-363 (1999); WO9932619). Genes causing altered phenotypes in the worms were identified as modifiers of the beta-catenin pathway. Accordingly, vertebrate orthologs of these modifiers, and preferably the human orthologs, MBCAT genes (i.e., nucleic acids and polypeptides) are attractive drug targets for the

treatment of pathologies associated with a defective beta-catenin signaling pathway, such as cancer. Table 1 (Example II) lists the modifiers and their orthologs.

In vitro and in vivo methods of assessing MBCAT function are provided herein. Modulation of the MBCAT or their respective binding partners is useful for understanding the association of the beta-catenin pathway and its members in normal and disease conditions and for developing diagnostics and therapeutic modalities for beta-catenin related pathologies. MBCAT-modulating agents that act by inhibiting or enhancing MBCAT expression, directly or indirectly, for example, by affecting an MBCAT function such as enzymatic (e.g., catalytic) or binding activity, can be identified using methods provided herein. MBCAT modulating agents are useful in diagnosis, therapy and pharmaceutical development.

Nucleic acids and polypeptides of the invention

Sequences related to MBCAT nucleic acids and polypeptides that can be used in the invention are disclosed in Genbank (referenced by Genbank identifier (GI) or RefSeq number), and shown in Table 1.

The term "MBCAT polypeptide" refers to a full-length MBCAT protein or a functionally active fragment or derivative thereof. A "functionally active" MBCAT fragment or derivative exhibits one or more functional activities associated with a full-length, wild-type MBCAT protein, such as antigenic or immunogenic activity, enzymatic activity, ability to bind natural cellular substrates, etc. The functional activity of MBCAT proteins, derivatives and fragments can be assayed by various methods known to one skilled in the art (Current Protocols in Protein Science (1998) Coligan *et al.*, eds., John Wiley & Sons, Inc., Somerset, New Jersey) and as further discussed below. In one embodiment, a functionally active MBCAT polypeptide is a MBCAT derivative capable of rescuing defective endogenous MBCAT activity, such as in cell based or animal assays; the rescuing derivative may be from the same or a different species. For purposes herein, functionally active fragments also include those fragments that comprise one or more structural domains of an MBCAT, such as a kinase domain or a binding domain. Protein domains can be identified using the PFAM program (Bateman A., et al., Nucleic Acids Res, 1999, 27:260-2). Methods for obtaining MBCAT polypeptides are also further described below. In some embodiments, preferred fragments are functionally active, domain-containing fragments comprising at least 25 contiguous amino acids, preferably at least 50, more preferably 75, and most preferably at least 100 contiguous amino acids of

any one of SEQ ID NOs:10-16 (an MBCAT). In further preferred embodiments, the fragment comprises the entire functionally active domain.

The term "MBCAT nucleic acid" refers to a DNA or RNA molecule that encodes a MBCAT polypeptide. Preferably, the MBCAT polypeptide or nucleic acid or fragment thereof is from a human, but can also be an ortholog, or derivative thereof with at least 70% sequence identity, preferably at least 80%, more preferably 85%, still more preferably 90%, and most preferably at least 95% sequence identity with human MBCAT. Methods of identifying orthlogs are known in the art. Normally, orthologs in different species retain the same function, due to presence of one or more protein motifs and/or 3-dimensional structures. Orthologs are generally identified by sequence homology analysis, such as BLAST analysis, usually using protein bait sequences. Sequences are assigned as a potential ortholog if the best hit sequence from the forward BLAST result retrieves the original query sequence in the reverse BLAST (Huynen MA and Bork P, Proc Natl Acad Sci (1998) 95:5849-5856; Huynen MA *et al.*, Genome Research (2000) 10:1204-1210). Programs for multiple sequence alignment, such as CLUSTAL (Thompson JD et al, 1994, Nucleic Acids Res 22:4673-4680) may be used to highlight conserved regions and/or residues of orthologous proteins and to generate phylogenetic trees. In a phylogenetic tree representing multiple homologous sequences from diverse species (e.g., retrieved through BLAST analysis), orthologous sequences from two species generally appear closest on the tree with respect to all other sequences from these two species. Structural threading or other analysis of protein folding (e.g., using software by ProCeryon, Biosciences, Salzburg, Austria) may also identify potential orthologs. In evolution, when a gene duplication event follows speciation, a single gene in one species, such as *C. elegans*, may correspond to multiple genes (paralogs) in another, such as human. As used herein, the term "orthologs" encompasses paralogs. As used herein, "percent (%) sequence identity" with respect to a subject sequence, or a specified portion of a subject sequence, is defined as the percentage of nucleotides or amino acids in the candidate derivative sequence identical with the nucleotides or amino acids in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul *et al.*, J. Mol. Biol. (1997) 215:403-410) with all the search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the

sequence of interest is being searched. A % identity value is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported. "Percent (%) amino acid sequence similarity" is determined by doing the same calculation as for determining % amino acid sequence identity, but including conservative amino acid substitutions in addition to identical amino acids in the computation.

A conservative amino acid substitution is one in which an amino acid is substituted for another amino acid having similar properties such that the folding or activity of the protein is not significantly affected. Aromatic amino acids that can be substituted for each other are phenylalanine, tryptophan, and tyrosine; interchangeable hydrophobic amino acids are leucine, isoleucine, methionine, and valine; interchangeable polar amino acids are glutamine and asparagine; interchangeable basic amino acids are arginine, lysine and histidine; interchangeable acidic amino acids are aspartic acid and glutamic acid; and interchangeable small amino acids are alanine, serine, threonine, cysteine and glycine.

Alternatively, an alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman (Smith and Waterman, 1981, Advances in Applied Mathematics 2:482-489; database: European Bioinformatics Institute; Smith and Waterman, 1981, J. of Molec.Biol., 147:195-197; Nicholas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (www.psc.edu) and references cited therein.; W.R. Pearson, 1991, Genomics 11:635-650). This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff (Dayhoff: Atlas of Protein Sequences and Structure, M. O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA), and normalized by Gribskov (Gribskov 1986 Nucl. Acids Res. 14(6):6745-6763). The Smith-Waterman algorithm may be employed where default parameters are used for scoring (for example, gap open penalty of 12, gap extension penalty of two). From the data generated, the "Match" value reflects "sequence identity."

Derivative nucleic acid molecules of the subject nucleic acid molecules include sequences that hybridize to the nucleic acid sequence of any of SEQ ID NOs:1-9. The stringency of hybridization can be controlled by temperature, ionic strength, pH, and the presence of denaturing agents such as formamide during hybridization and washing. Conditions routinely used are set out in readily available procedure texts (*e.g.*, Current Protocol in Molecular Biology, Vol. 1, Chap. 2.10, John Wiley & Sons, Publishers (1994); Sambrook *et al.*, Molecular Cloning, Cold Spring Harbor (1989)). In some embodiments,

a nucleic acid molecule of the invention is capable of hybridizing to a nucleic acid molecule containing the nucleotide sequence of any one of SEQ ID NOs:1-9 under high stringency hybridization conditions that are: prehybridization of filters containing nucleic acid for 8 hours to overnight at 65° C in a solution comprising 6X single strength citrate (SSC) (1X SSC is 0.15 M NaCl, 0.015 M Na citrate; pH 7.0), 5X Denhardt's solution, 0.05% sodium pyrophosphate and 100 μg/ml herring sperm DNA; hybridization for 18-20 hours at 65° C in a solution containing 6X SSC, 1X Denhardt's solution, 100 μg/ml yeast tRNA and 0.05% sodium pyrophosphate; and washing of filters at 65° C for 1h in a solution containing 0.1X SSC and 0.1% SDS (sodium dodecyl sulfate).

In other embodiments, moderately stringent hybridization conditions are used that are: pretreatment of filters containing nucleic acid for 6 h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 μg/ml denatured salmon sperm DNA; hybridization for 18-20h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 μg/ml salmon sperm DNA, and 10% (wt/vol) dextran sulfate; followed by washing twice for 1 hour at 55° C in a solution containing 2X SSC and 0.1% SDS.

Alternatively, low stringency conditions can be used that are: incubation for 8 hours to overnight at 37° C in a solution comprising 20% formamide, 5 x SSC, 50 mM sodium phosphate (pH 7.6), 5X Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured sheared salmon sperm DNA; hybridization in the same buffer for 18 to 20 hours; and washing of filters in 1 x SSC at about 37° C for 1 hour.

Isolation, Production, Expression, and Mis-expression of MBCAT Nucleic Acids and Polypeptides

MBCAT nucleic acids and polypeptides, useful for identifying and testing agents that modulate MBCAT function and for other applications related to the involvement of MBCAT in the beta-catenin pathway. MBCAT nucleic acids and derivatives and orthologs thereof may be obtained using any available method. For instance, techniques for isolating cDNA or genomic DNA sequences of interest by screening DNA libraries or by using polymerase chain reaction (PCR) are well known in the art. In general, the particular use for the protein will dictate the particulars of expression, production, and purification methods. For instance, production of proteins for use in screening for modulating agents may require methods that preserve specific biological activities of these

proteins, whereas production of proteins for antibody generation may require structural integrity of particular epitopes. Expression of proteins to be purified for screening or antibody production may require the addition of specific tags (*e.g.*, generation of fusion proteins). Overexpression of an MBCAT protein for assays used to assess MBCAT function, such as involvement in cell cycle regulation or hypoxic response, may require expression in eukaryotic cell lines capable of these cellular activities. Techniques for the expression, production, and purification of proteins are well known in the art; any suitable means therefore may be used (e.g., Higgins SJ and Hames BD (eds.) Protein Expression: A Practical Approach, Oxford University Press Inc., New York 1999; Stanbury PF et al., Principles of Fermentation Technology, 2nd edition, Elsevier Science, New York, 1995; Doonan S (ed.) Protein Purification Protocols, Humana Press, New Jersey, 1996; Coligan JE et al, Current Protocols in Protein Science (eds.), 1999, John Wiley & Sons, New York). In particular embodiments, recombinant MBCAT is expressed in a cell line known to have defective beta-catenin function. The recombinant cells are used in cell-based screening assay systems of the invention, as described further below.

The nucleotide sequence encoding an MBCAT polypeptide can be inserted into any appropriate expression vector. The necessary transcriptional and translational signals, including promoter/enhancer element, can derive from the native MBCAT gene and/or its flanking regions or can be heterologous. A variety of host-vector expression systems may be utilized, such as mammalian cell systems infected with virus (*e.g.* vaccinia virus, adenovirus, *etc.*); insect cell systems infected with virus (*e.g.* baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, plasmid, or cosmid DNA. An isolated host cell strain that modulates the expression of, modifies, and/or specifically processes the gene product may be used.

To detect expression of the MBCAT gene product, the expression vector can comprise a promoter operably linked to an MBCAT gene nucleic acid, one or more origins of replication, and, one or more selectable markers (*e.g.* thymidine kinase activity, resistance to antibiotics, *etc.*). Alternatively, recombinant expression vectors can be identified by assaying for the expression of the MBCAT gene product based on the physical or functional properties of the MBCAT protein in *in vitro* assay systems (*e.g.* immunoassays).

The MBCAT protein, fragment, or derivative may be optionally expressed as a fusion, or chimeric protein product (i.e. it is joined via a peptide bond to a heterologous protein sequence of a different protein), for example to facilitate purification or detection.

A chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other using standard methods and expressing the chimeric product. A chimeric product may also be made by protein synthetic techniques, *e.g.* by use of a peptide synthesizer (Hunkapiller *et al.*, Nature (1984) 310:105-111).

Once a recombinant cell that expresses the MBCAT gene sequence is identified, the gene product can be isolated and purified using standard methods (*e.g.* ion exchange, affinity, and gel exclusion chromatography; centrifugation; differential solubility; electrophoresis). Alternatively, native MBCAT proteins can be purified from natural sources, by standard methods (*e.g.* immunoaffinity purification). Once a protein is obtained, it may be quantified and its activity measured by appropriate methods, such as immunoassay, bioassay, or other measurements of physical properties, such as crystallography.

The methods of this invention may also use cells that have been engineered for altered expression (mis-expression) of MBCAT or other genes associated with the beta-catenin pathway. As used herein, mis-expression encompasses ectopic expression, over-expression, under-expression, and non-expression (*e.g.* by gene knock-out or blocking expression that would otherwise normally occur).

Genetically modified animals

Animal models that have been genetically modified to alter MBCAT expression may be used in *in vivo* assays to test for activity of a candidate beta-catenin modulating agent, or to further assess the role of MBCAT in a beta-catenin pathway process such as apoptosis or cell proliferation. Preferably, the altered MBCAT expression results in a detectable phenotype, such as decreased or increased levels of cell proliferation, angiogenesis, or apoptosis compared to control animals having normal MBCAT expression. The genetically modified animal may additionally have altered beta-catenin expression (e.g. beta-catenin knockout). Preferred genetically modified animals are mammals such as primates, rodents (preferably mice or rats), among others. Preferred non-mammalian species include zebrafish, *C. elegans*, and *Drosophila*. Preferred genetically modified animals are transgenic animals having a heterologous nucleic acid sequence present as an extrachromosomal element in a portion of its cells, i.e. mosaic animals (see, for example, techniques described by Jakobovits, 1994, Curr. Biol. 4:761-763.) or stably integrated into its germ line DNA (i.e., in the genomic sequence of most or

all of its cells). Heterologous nucleic acid is introduced into the germ line of such transgenic animals by genetic manipulation of, for example, embryos or embryonic stem cells of the host animal.

Methods of making transgenic animals are well-known in the art (for transgenic mice see Brinster et al., Proc. Nat. Acad. Sci. USA 82: 4438-4442 (1985), U.S. Pat. Nos. 4,736,866 and 4,870,009, both by Leder et al., U.S. Pat. No. 4,873,191 by Wagner et al., and Hogan, B., Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986); for particle bombardment see U.S. Pat. No., 4,945,050, by Sandford *et al.*; for transgenic *Drosophila* see Rubin and Spradling, Science (1982) 218:348-53 and U.S. Pat. No. 4,670,388; for transgenic insects see Berghammer A.J. *et al.*, A Universal Marker for Transgenic Insects (1999) Nature 402:370-371; for transgenic Zebrafish see Lin S., Transgenic Zebrafish, Methods Mol Biol. (2000);136:375-3830); for microinjection procedures for fish, amphibian eggs and birds see Houdebine and Chourrout, Experientia (1991) 47:897-905; for transgenic rats see Hammer *et al.*, Cell (1990) 63:1099-1112; and for culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection see, e.g., Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E. J. Robertson, ed., IRL Press (1987)). Clones of the nonhuman transgenic animals can be produced according to available methods (see Wilmut, I. *et al.* (1997) Nature 385:810-813; and PCT International Publication Nos. WO 97/07668 and WO 97/07669).

In one embodiment, the transgenic animal is a "knock-out" animal having a heterozygous or homozygous alteration in the sequence of an endogenous MBCAT gene that results in a decrease of MBCAT function, preferably such that MBCAT expression is undetectable or insignificant. Knock-out animals are typically generated by homologous recombination with a vector comprising a transgene having at least a portion of the gene to be knocked out. Typically a deletion, addition or substitution has been introduced into the transgene to functionally disrupt it. The transgene can be a human gene (e.g., from a human genomic clone) but more preferably is an ortholog of the human gene derived from the transgenic host species. For example, a mouse MBCAT gene is used to construct a homologous recombination vector suitable for altering an endogenous MBCAT gene in the mouse genome. Detailed methodologies for homologous recombination in mice are available (see Capecchi, Science (1989) 244:1288-1292; Joyner *et al.*, Nature (1989) 338:153-156). Procedures for the production of non-rodent transgenic mammals and other

animals are also available (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science (1989) 244:1281-1288; Simms *et al.*, Bio/Technology (1988) 6:179-183). In a preferred embodiment, knock-out animals, such as mice harboring a knockout of a specific gene, may be used to produce antibodies against the human counterpart of the gene that has been knocked out (Claesson MH et al., (1994) Scan J Immunol 40:257-264; Declerck PJ et al., (1995) J Biol Chem. 270:8397-400).

In another embodiment, the transgenic animal is a "knock-in" animal having an alteration in its genome that results in altered expression (e.g., increased (including ectopic) or decreased expression) of the MBCAT gene, e.g., by introduction of additional copies of MBCAT, or by operatively inserting a regulatory sequence that provides for altered expression of an endogenous copy of the MBCAT gene. Such regulatory sequences include inducible, tissue-specific, and constitutive promoters and enhancer elements. The knock-in can be homozygous or heterozygous.

Transgenic nonhuman animals can also be produced that contain selected systems allowing for regulated expression of the transgene. One example of such a system that may be produced is the cre/loxP recombinase system of bacteriophage P1 (Lakso *et al.*, PNAS (1992) 89:6232-6236; U.S. Pat. No. 4,959,317). If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase. Another example of a recombinase system is the FLP recombinase system of Saccharomyces cerevisiae (O'Gorman et al. (1991) Science 251:1351-1355; U.S. Pat. No. 5,654,182). In a preferred embodiment, both Cre-LoxP and Flp-Frt are used in the same system to regulate expression of the transgene, and for sequential deletion of vector sequences in the same cell (Sun X et al (2000) Nat Genet 25:83-6).

The genetically modified animals can be used in genetic studies to further elucidate the beta-catenin pathway, as animal models of disease and disorders implicating defective beta-catenin function, and for *in vivo* testing of candidate therapeutic agents, such as those identified in screens described below. The candidate therapeutic agents are administered to a genetically modified animal having altered MBCAT function and phenotypic changes are compared with appropriate control animals such as genetically modified animals that

receive placebo treatment, and/or animals with unaltered MBCAT expression that receive candidate therapeutic agent.

In addition to the above-described genetically modified animals having altered MBCAT function, animal models having defective beta-catenin function (and otherwise normal MBCAT function), can be used in the methods of the present invention. For example, a beta-catenin knockout mouse can be used to assess, *in vivo*, the activity of a candidate beta-catenin modulating agent identified in one of the *in vitro* assays described below. Preferably, the candidate beta-catenin modulating agent when administered to a model system with cells defective in beta-catenin function, produces a detectable phenotypic change in the model system indicating that the beta-catenin function is restored, i.e., the cells exhibit normal cell cycle progression.

Modulating Agents

The invention provides methods to identify agents that interact with and/or modulate the function of MBCAT and/or the beta-catenin pathway. Modulating agents identified by the methods are also part of the invention. Such agents are useful in a variety of diagnostic and therapeutic applications associated with the beta-catenin pathway, as well as in further analysis of the MBCAT protein and its contribution to the beta-catenin pathway. Accordingly, the invention also provides methods for modulating the beta-catenin pathway comprising the step of specifically modulating MBCAT activity by administering a MBCAT-interacting or -modulating agent.

As used herein, an "MBCAT-modulating agent" is any agent that modulates MBCAT function, for example, an agent that interacts with MBCAT to inhibit or enhance MBCAT activity or otherwise affect normal MBCAT function. MBCAT function can be affected at any level, including transcription, protein expression, protein localization, and cellular or extra-cellular activity. In a preferred embodiment, the MBCAT - modulating agent specifically modulates the function of the MBCAT. The phrases "specific modulating agent", "specifically modulates", etc., are used herein to refer to modulating agents that directly bind to the MBCAT polypeptide or nucleic acid, and preferably inhibit, enhance, or otherwise alter, the function of the MBCAT. These phrases also encompasses modulating agents that alter the interaction of the MBCAT with a binding partner, substrate, or cofactor (e.g. by binding to a binding partner of an MBCAT, or to a protein/binding partner complex, and altering MBCAT function). In a further preferred embodiment, the MBCAT- modulating agent is a modulator of the beta-catenin pathway

(e.g. it restores and/or upregulates beta-catenin function) and thus is also a beta-catenin-modulating agent.

Preferred MBCAT-modulating agents include small molecule compounds; MBCAT-interacting proteins, including antibodies and other biotherapeutics; and nucleic acid modulators such as antisense and RNA inhibitors. The modulating agents may be formulated in pharmaceutical compositions, for example, as compositions that may comprise other active ingredients, as in combination therapy, and/or suitable carriers or excipients. Techniques for formulation and administration of the compounds may be found in "Remington's Pharmaceutical Sciences" Mack Publishing Co., Easton, PA, 19th edition.

Small molecule modulators

Small molecules are often preferred to modulate function of proteins with enzymatic function, and/or containing protein interaction domains. Chemical agents, referred to in the art as "small molecule" compounds are typically organic, non-peptide molecules, having a molecular weight less than 10,000, preferably less than 5,000, more preferably less than 1,000, and most preferably less than 500. This class of modulators includes chemically synthesized molecules, for instance, compounds from combinatorial chemical libraries. Synthetic compounds may be rationally designed or identified based on known or inferred properties of the MBCAT protein or may be identified by screening compound libraries. Alternative appropriate modulators of this class are natural products, particularly secondary metabolites from organisms such as plants or fungi, which can also be identified by screening compound libraries for MBCAT–modulating activity. Methods for generating and obtaining compounds are well known in the art (Schreiber SL, Science (2000) 151: 1964-1969; Radmann J and Gunther J, Science (2000) 151:1947-1948).

Small molecule modulators identified from screening assays, as described below, can be used as lead compounds from which candidate clinical compounds may be designed, optimized, and synthesized. Such clinical compounds may have utility in treating pathologies associated with the beta-catenin pathway. The activity of candidate small molecule modulating agents may be improved several-fold through iterative secondary functional validation, as further described below, structure determination, and candidate modulator modification and testing. Additionally, candidate clinical compounds are generated with specific regard to clinical and pharmacological properties. For example,

the reagents may be derivatized and re-screened using *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development.

Protein Modulators

Specific MBCAT-interacting proteins are useful in a variety of diagnostic and therapeutic applications related to the beta-catenin pathway and related disorders, as well as in validation assays for other MBCAT-modulating agents. In a preferred embodiment, MBCAT-interacting proteins affect normal MBCAT function, including transcription, protein expression, protein localization, and cellular or extra-cellular activity. In another embodiment, MBCAT-interacting proteins are useful in detecting and providing information about the function of MBCAT proteins, as is relevant to beta-catenin related disorders, such as cancer (e.g., for diagnostic means).

An MBCAT-interacting protein may be endogenous, i.e. one that naturally interacts genetically or biochemically with an MBCAT, such as a member of the MBCAT pathway that modulates MBCAT expression, localization, and/or activity. MBCAT-modulators include dominant negative forms of MBCAT-interacting proteins and of MBCAT proteins themselves. Yeast two-hybrid and variant screens offer preferred methods for identifying endogenous MBCAT-interacting proteins (Finley, R. L. et al. (1996) in DNA Cloning-Expression Systems: A Practical Approach, eds. Glover D. & Hames B. D (Oxford University Press, Oxford, England), pp. 169-203; Fashema SF et al., Gene (2000) 250:1-14; Drees BL Curr Opin Chem Biol (1999) 3:64-70; Vidal M and Legrain P Nucleic Acids Res (1999) 27:919-29; and U.S. Pat. No. 5,928,868). Mass spectrometry is an alternative preferred method for the elucidation of protein complexes (reviewed in, e.g., Pandley A and Mann M, Nature (2000) 405:837-846; Yates JR 3rd, Trends Genet (2000) 16:5-8).

An MBCAT-interacting protein may be an exogenous protein, such as an MBCAT-specific antibody or a T-cell antigen receptor (see, e.g., Harlow and Lane (1988) Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory; Harlow and Lane (1999) Using antibodies: a laboratory manual. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press). MBCAT antibodies are further discussed below.

In preferred embodiments, an MBCAT-interacting protein specifically binds an MBCAT protein. In alternative preferred embodiments, an MBCAT-modulating agent binds an MBCAT substrate, binding partner, or cofactor.

Antibodies

In another embodiment, the protein modulator is an MBCAT specific antibody agonist or antagonist. The antibodies have therapeutic and diagnostic utilities, and can be used in screening assays to identify MBCAT modulators. The antibodies can also be used in dissecting the portions of the MBCAT pathway responsible for various cellular responses and in the general processing and maturation of the MBCAT.

Antibodies that specifically bind MBCAT polypeptides can be generated using known methods. Preferably the antibody is specific to a mammalian ortholog of MBCAT polypeptide, and more preferably, to human MBCAT. Antibodies may be polyclonal, monoclonal (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab').sub.2 fragments, fragments produced by a FAb expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Epitopes of MBCAT which are particularly antigenic can be selected, for example, by routine screening of MBCAT polypeptides for antigenicity or by applying a theoretical method for selecting antigenic regions of a protein (Hopp and Wood (1981), Proc. Nati. Acad. Sci. U.S.A. 78:3824-28; Hopp and Wood, (1983) Mol. Immunol. 20:483-89; Sutcliffe et al., (1983) Science 219:660-66) to the amino acid sequence shown in any of SEQ ID NOs:10-16. Monoclonal antibodies with affinities of 10^8 M^{-1} preferably 10^9 M^{-1} to 10^{10} M^{-1}, or stronger can be made by standard procedures as described (Harlow and Lane, *supra*; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed) Academic Press, New York; and U.S. Pat. Nos. 4,381,292; 4,451,570; and 4,618,577). Antibodies may be generated against crude cell extracts of MBCAT or substantially purified fragments thereof. If MBCAT fragments are used, they preferably comprise at least 10, and more preferably, at least 20 contiguous amino acids of an MBCAT protein. In a particular embodiment, MBCAT-specific antigens and/or immunogens are coupled to carrier proteins that stimulate the immune response. For example, the subject polypeptides are covalently coupled to the keyhole limpet hemocyanin (KLH) carrier, and the conjugate is emulsified in Freund's complete adjuvant, which enhances the immune response. An appropriate immune system such as a laboratory rabbit or mouse is immunized according to conventional protocols.

The presence of MBCAT-specific antibodies is assayed by an appropriate assay such as a solid phase enzyme-linked immunosorbant assay (ELISA) using immobilized corresponding MBCAT polypeptides. Other assays, such as radioimmunoassays or fluorescent assays might also be used.

Chimeric antibodies specific to MBCAT polypeptides can be made that contain different portions from different animal species. For instance, a human immunoglobulin constant region may be linked to a variable region of a murine mAb, such that the antibody derives its biological activity from the human antibody, and its binding specificity from the murine fragment. Chimeric antibodies are produced by splicing together genes that encode the appropriate regions from each species (Morrison et al., Proc. Natl. Acad. Sci. (1984) 81:6851-6855; Neuberger et al., Nature (1984) 312:604-608; Takeda et al., Nature (1985) 31:452-454). Humanized antibodies, which are a form of chimeric antibodies, can be generated by grafting complementary-determining regions (CDRs) (Carlos, T. M., J. M. Harlan. 1994. Blood 84:2068-2101) of mouse antibodies into a background of human framework regions and constant regions by recombinant DNA technology (Riechmann LM, et al., 1988 Nature 323: 323-327). Humanized antibodies contain ~10% murine sequences and ~90% human sequences, and thus further reduce or eliminate immunogenicity, while retaining the antibody specificities (Co MS, and Queen C. 1991 Nature 351: 501-501; Morrison SL. 1992 Ann. Rev. Immun. 10:239-265). Humanized antibodies and methods of their production are well-known in the art (U.S. Pat. Nos. 5,530,101, 5,585,089, 5,693,762, and 6,180,370).

MBCAT-specific single chain antibodies which are recombinant, single chain polypeptides formed by linking the heavy and light chain fragments of the Fv regions via an amino acid bridge, can be produced by methods known in the art (U.S. Pat. No. 4,946,778; Bird, Science (1988) 242:423-426; Huston et al., Proc. Natl. Acad. Sci. USA (1988) 85:5879-5883; and Ward et al., Nature (1989) 334:544-546).

Other suitable techniques for antibody production involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors (Huse et al., Science (1989) 246:1275-1281). As used herein, T-cell antigen receptors are included within the scope of antibody modulators (Harlow and Lane, 1988, *supra*).

The polypeptides and antibodies of the present invention may be used with or without modification. Frequently, antibodies will be labeled by joining, either covalently or non-covalently, a substance that provides for a detectable signal, or that is toxic to cells that express the targeted protein (Menard S, et al., Int J. Biol Markers (1989) 4:131-134). A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, fluorescent

emitting lanthanide metals, chemiluminescent moieties, bioluminescent moieties, magnetic particles, and the like (U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241). Also, recombinant immunoglobulins may be produced (U.S. Pat. No. 4,816,567). Antibodies to cytoplasmic polypeptides may be delivered and reach their targets by conjugation with membrane-penetrating toxin proteins (U.S. Pat. No. 6,086,900).

When used therapeutically in a patient, the antibodies of the subject invention are typically administered parenterally, when possible at the target site, or intravenously. The therapeutically effective dose and dosage regimen is determined by clinical studies. Typically, the amount of antibody administered is in the range of about 0.1 mg/kg –to about 10 mg/kg of patient weight. For parenteral administration, the antibodies are formulated in a unit dosage injectable form (e.g., solution, suspension, emulsion) in association with a pharmaceutically acceptable vehicle. Such vehicles are inherently nontoxic and non-therapeutic. Examples are water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Nonaqueous vehicles such as fixed oils, ethyl oleate, or liposome carriers may also be used. The vehicle may contain minor amounts of additives, such as buffers and preservatives, which enhance isotonicity and chemical stability or otherwise enhance therapeutic potential. The antibodies' concentrations in such vehicles are typically in the range of about 1 mg/ml to about10 mg/ml. Immunotherapeutic methods are further described in the literature (US Pat. No. 5,859,206; WO0073469).

Specific biotherapeutics

In a preferred embodiment, an MBCAT-interacting protein may have biotherapeutic applications. Biotherapeutic agents formulated in pharmaceutically acceptable carriers and dosages may be used to activate or inhibit signal transduction pathways. This modulation may be accomplished by binding a ligand, thus inhibiting the activity of the pathway; or by binding a receptor, either to inhibit activation of, or to activate, the receptor. Alternatively, the biotherapeutic may itself be a ligand capable of activating or inhibiting a receptor. Biotherapeutic agents and methods of producing them are described in detail in U.S. Pat. No. 6,146,628.

When the MBCAT is a ligand, it may be used as a biotherapeutic agent to activate or inhibit its natural receptor. Alternatively, antibodies against MBCAT, as described in the previous section, may be used as biotherapeutic agents.

When the MBCAT is a receptor, its ligand(s), antibodies to the ligand(s) or the MBCAT itself may be used as biotherapeutics to modulate the activity of MBCAT in the beta-catenin pathway.

Nucleic Acid Modulators

Other preferred MBCAT-modulating agents comprise nucleic acid molecules, such as antisense oligomers or double stranded RNA (dsRNA), which generally inhibit MBCAT activity. Preferred nucleic acid modulators interfere with the function of the MBCAT nucleic acid such as DNA replication, transcription, translocation of the MBCAT RNA to the site of protein translation, translation of protein from the MBCAT RNA, splicing of the MBCAT RNA to yield one or more mRNA species, or catalytic activity which may be engaged in or facilitated by the MBCAT RNA.

In one embodiment, the antisense oligomer is an oligonucleotide that is sufficiently complementary to an MBCAT mRNA to bind to and prevent translation, preferably by binding to the 5′ untranslated region. MBCAT-specific antisense oligonucleotides, preferably range from at least 6 to about 200 nucleotides. In some embodiments the oligonucleotide is preferably at least 10, 15, or 20 nucleotides in length. In other embodiments, the oligonucleotide is preferably less than 50, 40, or 30 nucleotides in length. The oligonucleotide can be DNA or RNA or a chimeric mixture or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents that facilitate transport across the cell membrane, hybridization-triggered cleavage agents, and intercalating agents.

In another embodiment, the antisense oligomer is a phosphothioate morpholino oligomer (PMO). PMOs are assembled from four different morpholino subunits, each of which contain one of four genetic bases (A, C, G, or T) linked to a six-membered morpholine ring. Polymers of these subunits are joined by non-ionic phosphodiamidate intersubunit linkages. Details of how to make and use PMOs and other antisense oligomers are well known in the art (e.g. see WO99/18193; Probst JC, Antisense Oligodeoxynucleotide and Ribozyme Design, Methods. (2000) 22(3):271-281; Summerton J, and Weller D. 1997 Antisense Nucleic Acid Drug Dev. :7:187-95; US Pat. No. 5,235,033; and US Pat No. 5,378,841).

Alternative preferred MBCAT nucleic acid modulators are double-stranded RNA species mediating RNA interference (RNAi). RNAi is the process of sequence-specific, post-transcriptional gene silencing in animals and plants, initiated by double-stranded RNA (dsRNA) that is homologous in sequence to the silenced gene. Methods relating to the use of RNAi to silence genes in *C. elegans*, *Drosophila*, plants, and humans are known in the art (Fire A, et al., 1998 Nature 391:806-811; Fire, A. Trends Genet. 15, 358-363 (1999); Sharp, P. A. RNA interference 2001. Genes Dev. 15, 485-490 (2001); Hammond, S. M., et al., Nature Rev. Genet. 2, 110-1119 (2001); Tuschl, T. Chem. Biochem. 2, 239-245 (2001); Hamilton, A. et al., Science 286, 950-952 (1999); Hammond, S. M., et al., Nature 404, 293-296 (2000); Zamore, P. D., et al., Cell 101, 25-33 (2000); Bernstein, E., et al., Nature 409, 363-366 (2001); Elbashir, S. M., et al., Genes Dev. 15, 188-200 (2001); WO0129058; WO9932619; Elbashir SM, et al., 2001 Nature 411:494-498).

Nucleic acid modulators are commonly used as research reagents, diagnostics, and therapeutics. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used to elucidate the function of particular genes (see, for example, U.S. Pat. No. 6,165,790). Nucleic acid modulators are also used, for example, to distinguish between functions of various members of a biological pathway. For example, antisense oligomers have been employed as therapeutic moieties in the treatment of disease states in animals and man and have been demonstrated in numerous clinical trials to be safe and effective (Milligan JF, *et al*, Current Concepts in Antisense Drug Design, J Med Chem. (1993) 36:1923-1937; Tonkinson JL *et al.*, Antisense Oligodeoxynucleotides as Clinical Therapeutic Agents, Cancer Invest. (1996) 14:54-65). Accordingly, in one aspect of the invention, an MBCAT-specific nucleic acid modulator is used in an assay to further elucidate the role of the MBCAT in the beta-catenin pathway, and/or its relationship to other members of the pathway. In another aspect of the invention, an MBCAT-specific antisense oligomer is used as a therapeutic agent for treatment of beta-catenin-related disease states.

Assay Systems

The invention provides assay systems and screening methods for identifying specific modulators of MBCAT activity. As used herein, an "assay system" encompasses all the components required for performing and analyzing results of an assay that detects and/or measures a particular event. In general, primary assays are used to identify or confirm a modulator's specific biochemical or molecular effect with respect to the

MBCAT nucleic acid or protein. In general, secondary assays further assess the activity of a MBCAT modulating agent identified by a primary assay and may confirm that the modulating agent affects MBCAT in a manner relevant to the beta-catenin pathway. In some cases, MBCAT modulators will be directly tested in a secondary assay.

In a preferred embodiment, the screening method comprises contacting a suitable assay system comprising an MBCAT polypeptide or nucleic acid with a candidate agent under conditions whereby, but for the presence of the agent, the system provides a reference activity (e.g. binding activity), which is based on the particular molecular event the screening method detects. A statistically significant difference between the agent-biased activity and the reference activity indicates that the candidate agent modulates MBCAT activity, and hence the beta-catenin pathway. The MBCAT polypeptide or nucleic acid used in the assay may comprise any of the nucleic acids or polypeptides described above.

Primary Assays

The type of modulator tested generally determines the type of primary assay.

Primary assays for small molecule modulators

For small molecule modulators, screening assays are used to identify candidate modulators. Screening assays may be cell-based or may use a cell-free system that recreates or retains the relevant biochemical reaction of the target protein (reviewed in Sittampalam GS *et al.*, Curr Opin Chem Biol (1997) 1:384-91 and accompanying references). As used herein the term "cell-based" refers to assays using live cells, dead cells, or a particular cellular fraction, such as a membrane, endoplasmic reticulum, or mitochondrial fraction. The term "cell free" encompasses assays using substantially purified protein (either endogenous or recombinantly produced), partially purified or crude cellular extracts. Screening assays may detect a variety of molecular events, including protein-DNA interactions, protein-protein interactions (*e.g.*, receptor-ligand binding), transcriptional activity (*e.g.*, using a reporter gene), enzymatic activity (*e.g.*, via a property of the substrate), activity of second messengers, immunogenicty and changes in cellular morphology or other cellular characteristics. Appropriate screening assays may use a wide range of detection methods including fluorescent, radioactive, colorimetric, spectrophotometric, and amperometric methods, to provide a read-out for the particular molecular event detected.

Cell-based screening assays usually require systems for recombinant expression of MBCAT and any auxiliary proteins demanded by the particular assay. Appropriate methods for generating recombinant proteins produce sufficient quantities of proteins that retain their relevant biological activities and are of sufficient purity to optimize activity and assure assay reproducibility. Yeast two-hybrid and variant screens, and mass spectrometry provide preferred methods for determining protein-protein interactions and elucidation of protein complexes. In certain applications, when MBCAT-interacting proteins are used in screens to identify small molecule modulators, the binding specificity of the interacting protein to the MBCAT protein may be assayed by various known methods such as substrate processing (e.g. ability of the candidate MBCAT-specific binding agents to function as negative effectors in MBCAT-expressing cells), binding equilibrium constants (usually at least about 10^7 M^{-1}, preferably at least about 10^8 M^{-1}, more preferably at least about 10^9 M^{-1}), and immunogenicity (e.g. ability to elicit MBCAT specific antibody in a heterologous host such as a mouse, rat, goat or rabbit). For enzymes and receptors, binding may be assayed by, respectively, substrate and ligand processing.

The screening assay may measure a candidate agent's ability to specifically bind to or modulate activity of a MBCAT polypeptide, a fusion protein thereof, or to cells or membranes bearing the polypeptide or fusion protein. The MBCAT polypeptide can be full length or a fragment thereof that retains functional MBCAT activity. The MBCAT polypeptide may be fused to another polypeptide, such as a peptide tag for detection or anchoring, or to another tag. The MBCAT polypeptide is preferably human MBCAT, or is an ortholog or derivative thereof as described above. In a preferred embodiment, the screening assay detects candidate agent-based modulation of MBCAT interaction with a binding target, such as an endogenous or exogenous protein or other substrate that has MBCAT –specific binding activity, and can be used to assess normal MBCAT gene function.

Suitable assay formats that may be adapted to screen for MBCAT modulators are known in the art. Preferred screening assays are high throughput or ultra high throughput and thus provide automated, cost-effective means of screening compound libraries for lead compounds (Fernandes PB, Curr Opin Chem Biol (1998) 2:597-603; Sundberg SA, Curr Opin Biotechnol 2000, 11:47-53). In one preferred embodiment, screening assays uses fluorescence technologies, including fluorescence polarization, time-resolved fluorescence, and fluorescence resonance energy transfer. These systems offer means to monitor protein-protein or DNA-protein interactions in which the intensity of the signal

emitted from dye-labeled molecules depends upon their interactions with partner molecules (*e.g.*, Selvin PR, Nat Struct Biol (2000) 7:730-4; Fernandes PB, *supra*; Hertzberg RP and Pope AJ, Curr Opin Chem Biol (2000) 4:445-451).

A variety of suitable assay systems may be used to identify candidate MBCAT and beta-catenin pathway modulators (e.g. U.S. Pat. No. 6,165,992 (kinase assays); U.S. Pat. Nos. 5,550,019 and 6,133,437 (apoptosis assays); U.S. Pat. Nos. 5,976,782, 6,225,118 and 6,444,434 (angiogenesis assays), among others). Specific preferred assays are described in more detail below.

Protein kinases, key signal transduction proteins that may be either membrane-associated or intracellular, catalyze the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. Radioassays, which monitor the transfer from [gamma-^{32}P or -^{33}P]ATP, are frequently used to assay kinase activity. For instance, a scintillation assay for p56 (lck) kinase activity monitors the transfer of the gamma phosphate from [gamma -^{33}P] ATP to a biotinylated peptide substrate. The substrate is captured on a streptavidin coated bead that transmits the signal (Beveridge M *et al.*, J Biomol Screen (2000) 5:205-212). This assay uses the scintillation proximity assay (SPA), in which only radio-ligand bound to receptors tethered to the surface of an SPA bead are detected by the scintillant immobilized within it, allowing binding to be measured without separation of bound from free ligand. Other assays for protein kinase activity may use antibodies that specifically recognize phosphorylated substrates. For instance, the kinase receptor activation (KIRA) assay measures receptor tyrosine kinase activity by ligand stimulating the intact receptor in cultured cells, then capturing solubilized receptor with specific antibodies and quantifying phosphorylation via phosphotyrosine ELISA (Sadick MD, Dev Biol Stand (1999) 97:121-133). Another example of antibody based assays for protein kinase activity is TRF (time-resolved fluorometry). This method utilizes europium chelate-labeled anti-phosphotyrosine antibodies to detect phosphate transfer to a polymeric substrate coated onto microtiter plate wells. The amount of phosphorylation is then detected using time-resolved, dissociation-enhanced fluorescence (Braunwalder AF, et al., Anal Biochem 1996 Jul 1;238(2):159-64).

Adapter proteins are involved in a wide range of signaling and other cellular processes and generally facilitate protein-protein or protein-nucleic acid interactions via certain conserved motifs, including PDZ, SH2, SH3, PH, TRAF, WD40, LIM, ankyrin repeat, KH and annexin domains, etc. Assays for adapter protein activity may measure

protein binding at the conserved motifs. For instance, exemplary assays for SH2 domain-containing proteins have measured binding using fluorescently labeled peptide substrate and fluorescence polarization or laser-scanning techniques (Lynch BA et al., Anal Biochem 1999, 275:62-73; Zuck P et al., Proc Natl Acad Sci USA 1999, 96: 11122-11127). An alternative SH2 binding assay uses radiolabeled peptide. An assay for protein-protein interaction at the LIM domain has used fluorescently labeled LIM-containing proteins (FHL2 and FHL3) and the fluorescence resonance energy transfer (FRET) technique (Li HY, J Cell Biochem 2001, 80:293-303).

Apoptosis assays. Assays for apoptosis may be performed by terminal deoxynucleotidyl transferase-mediated digoxigenin-11-dUTP nick end labeling (TUNEL) assay. The TUNEL assay is used to measure nuclear DNA fragmentation characteristic of apoptosis (Lazebnik *et al.*, 1994, Nature 371, 346), by following the incorporation of fluorescein-dUTP (Yonehara *et al.*, 1989, J. Exp. Med. 169, 1747). Apoptosis may further be assayed by acridine orange staining of tissue culture cells (Lucas, R., et al., 1998, Blood 15:4730-41). An apoptosis assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the apoptosis assay system and changes in induction of apoptosis relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, an apoptosis assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using a cell-free assay system. An apoptosis assay may also be used to test whether MBCAT function plays a direct role in apoptosis. For example, an apoptosis assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in apoptotic response compared to wild type cells suggests that the MBCAT plays a direct role in the apoptotic response. Apoptosis assays are described further in US Pat. No. 6,133,437.

Cell proliferation and cell cycle assays. Cell proliferation may be assayed via bromodeoxyuridine (BRDU) incorporation. This assay identifies a cell population undergoing DNA synthesis by incorporation of BRDU into newly-synthesized DNA. Newly-synthesized DNA may then be detected using an anti-BRDU antibody (Hoshino *et al.*, 1986, Int. J. Cancer 38, 369; Campana *et al.*, 1988, J. Immunol. Meth. 107, 79), or by other means.

Cell Proliferation may also be examined using [^{3}H]-thymidine incorporation (Chen, J., 1996, Oncogene 13:1395-403; Jeoung, J., 1995, J. Biol. Chem. 270:18367-73). This assay allows for quantitative characterization of S-phase DNA syntheses. In this assay, cells synthesizing DNA will incorporate [^{3}H]-thymidine into newly synthesized DNA. Incorporation can then be measured by standard techniques such as by counting of radioisotope in a scintillation counter (e.g., Beckman LS 3800 Liquid Scintillation Counter). Another proliferation assay uses the dye Alamar Blue (available from Biosource International), which fluoresces when reduced in living cells and provides an indirect measurement of cell number (Voytik-Harbin SL et al., 1998, In Vitro Cell Dev Biol Anim 34:239-46).

Cell proliferation may also be assayed by colony formation in soft agar (Sambrook et al., Molecular Cloning, Cold Spring Harbor (1989)). For example, cells transformed with MBCAT are seeded in soft agar plates, and colonies are measured and counted after two weeks incubation.

Involvement of a gene in the cell cycle may be assayed by flow cytometry (Gray JW et al. (1986) Int J Radiat Biol Relat Stud Phys Chem Med 49:237-55). Cells transfected with an MBCAT may be stained with propidium iodide and evaluated in a flow cytometer (available from Becton Dickinson), which indicates accumulation of cells in different stages of the cell cycle.

Accordingly, a cell proliferation or cell cycle assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the assay system and changes in cell proliferation or cell cycle relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, the cell proliferation or cell cycle assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using another assay system such as a cell-free assay system. A cell proliferation assay may also be used to test whether MBCAT function plays a direct role in cell proliferation or cell cycle. For example, a cell proliferation or cell cycle assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in proliferation or cell cycle compared to wild type cells suggests that the MBCAT plays a direct role in cell proliferation or cell cycle.

Angiogenesis. Angiogenesis may be assayed using various human endothelial cell systems, such as umbilical vein, coronary artery, or dermal cells. Suitable assays include Alamar Blue based assays (available from Biosource International) to measure proliferation; migration assays using fluorescent molecules, such as the use of Becton Dickinson Falcon HTS FluoroBlock cell culture inserts to measure migration of cells through membranes in presence or absence of angiogenesis enhancer or suppressors; and tubule formation assays based on the formation of tubular structures by endothelial cells on Matrigel® (Becton Dickinson). Accordingly, an angiogenesis assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the angiogenesis assay system and changes in angiogenesis relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, the angiogenesis assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using another assay system. An angiogenesis assay may also be used to test whether MBCAT function plays a direct role in cell proliferation. For example, an angiogenesis assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in angiogenesis compared to wild type cells suggests that the MBCAT plays a direct role in angiogenesis. U.S. Pat. Nos. 5,976,782, 6,225,118 and 6,444,434, among others.

Hypoxic induction. The alpha subunit of the transcription factor, hypoxia inducible factor-1 (HIF-1), is upregulated in tumor cells following exposure to hypoxia in vitro. Under hypoxic conditions, HIF-1 stimulates the expression of genes known to be important in tumour cell survival, such as those encoding glyolytic enzymes and VEGF. Induction of such genes by hypoxic conditions may be assayed by growing cells transfected with MBCAT in hypoxic conditions (such as with 0.1% O2, 5% CO2, and balance N2, generated in a Napco 7001 incubator (Precision Scientific)) and normoxic conditions, followed by assessment of gene activity or expression by Taqman®. For example, a hypoxic induction assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the hypoxic induction assay system and changes in hypoxic response relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some

embodiments of the invention, the hypoxic induction assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using another assay system. A hypoxic induction assay may also be used to test whether MBCAT function plays a direct role in the hypoxic response. For example, a hypoxic induction assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in hypoxic response compared to wild type cells suggests that the MBCAT plays a direct role in hypoxic induction.

Cell adhesion. Cell adhesion assays measure adhesion of cells to purified adhesion proteins, or adhesion of cells to each other, in presence or absence of candidate modulating agents. Cell-protein adhesion assays measure the ability of agents to modulate the adhesion of cells to purified proteins. For example, recombinant proteins are produced, diluted to 2.5g/mL in PBS, and used to coat the wells of a microtiter plate. The wells used for negative control are not coated. Coated wells are then washed, blocked with 1% BSA, and washed again. Compounds are diluted to 2× final test concentration and added to the blocked, coated wells. Cells are then added to the wells, and the unbound cells are washed off. Retained cells are labeled directly on the plate by adding a membrane-permeable fluorescent dye, such as calcein-AM, and the signal is quantified in a fluorescent microplate reader.

Cell-cell adhesion assays measure the ability of agents to modulate binding of cell adhesion proteins with their native ligands. These assays use cells that naturally or recombinantly express the adhesion protein of choice. In an exemplary assay, cells expressing the cell adhesion protein are plated in wells of a multiwell plate. Cells expressing the ligand are labeled with a membrane-permeable fluorescent dye, such as BCECF , and allowed to adhere to the monolayers in the presence of candidate agents. Unbound cells are washed off, and bound cells are detected using a fluorescence plate reader.

High-throughput cell adhesion assays have also been described. In one such assay, small molecule ligands and peptides are bound to the surface of microscope slides using a microarray spotter, intact cells are then contacted with the slides, and unbound cells are washed off. In this assay, not only the binding specificity of the peptides and modulators against cell lines are determined, but also the functional cell signaling of attached cells using immunofluorescence techniques in situ on the microchip is measured (Falsey JR et al., Bioconjug Chem. 2001 May-Jun;12(3):346-53).

Tubulogenesis. Tubulogenesis assays monitor the ability of cultured cells, generally endothelial cells, to form tubular structures on a matrix substrate, which generally simulates the environment of the extracellular matrix. Exemplary substrates include Matrigel™ (Becton Dickinson), an extract of basement membrane proteins containing laminin, collagen IV, and heparin sulfate proteoglycan, which is liquid at 4° C and forms a solid gel at 37° C. Other suitable matrices comprise extracellular components such as collagen, fibronectin, and/or fibrin. Cells are stimulated with a pro-angiogenic stimulant, and their ability to form tubules is detected by imaging. Tubules can generally be detected after an overnight incubation with stimuli, but longer or shorter time frames may also be used. Tube formation assays are well known in the art (e.g., Jones MK et al., 1999, Nature Medicine 5:1418-1423). These assays have traditionally involved stimulation with serum or with the growth factors FGF or VEGF. Serum represents an undefined source of growth factors. In a preferred embodiment, the assay is performed with cells cultured in serum free medium, in order to control which process or pathway a candidate agent modulates. Moreover, we have found that different target genes respond differently to stimulation with different pro-angiogenic agents, including inflammatory angiogenic factors such as TNF-alpa. Thus, in a further preferred embodiment, a tubulogenesis assay system comprises testing an MBCAT's response to a variety of factors, such as FGF, VEGF, phorbol myristate acetate (PMA), TNF-alpha, ephrin, etc.

Cell Migration. An invasion/migration assay (also called a migration assay) tests the ability of cells to overcome a physical barrier and to migrate towards pro-angiogenic signals. Migration assays are known in the art (e.g., Paik JH et al., 2001, J Biol Chem 276:11830-11837). In a typical experimental set-up, cultured endothelial cells are seeded onto a matrix-coated porous lamina, with pore sizes generally smaller than typical cell size. The matrix generally simulates the environment of the extracellular matrix, as described above. The lamina is typically a membrane, such as the transwell polycarbonate membrane (Corning Costar Corporation, Cambridge, MA), and is generally part of an upper chamber that is in fluid contact with a lower chamber containing pro-angiogenic stimuli. Migration is generally assayed after an overnight incubation with stimuli, but longer or shorter time frames may also be used. Migration is assessed as the number of cells that crossed the lamina, and may be detected by staining cells with hemotoxylin solution (VWR Scientific, South San Francisco, CA), or by any other method for determining cell number. In another exemplary set up, cells are fluorescently labeled and

migration is detected using fluorescent readings, for instance using the Falcon HTS FluoroBlok (Becton Dickinson). While some migration is observed in the absence of stimulus, migration is greatly increased in response to pro-angiogenic factors. As described above, a preferred assay system for migration/invasion assays comprises testing an MBCAT's response to a variety of pro-angiogenic factors, including tumor angiogenic and inflammatory angiogenic agents, and culturing the cells in serum free medium.

Sprouting assay. A sprouting assay is a three-dimensional *in vitro* angiogenesis assay that uses a cell-number defined spheroid aggregation of endothelial cells ("spheroid"), embedded in a collagen gel-based matrix. The spheroid can serve as a starting point for the sprouting of capillary-like structures by invasion into the extracellular matrix (termed "cell sprouting") and the subsequent formation of complex anastomosing networks (Korff and Augustin, 1999, J Cell Sci 112:3249-58). In an exemplary experimental set-up, spheroids are prepared by pipetting 400 human umbilical vein endothelial cells into individual wells of a nonadhesive 96-well plates to allow overnight spheroidal aggregation (Korff and Augustin: J Cell Biol 143: 1341-52, 1998). Spheroids are harvested and seeded in 900μl of methocel-collagen solution and pipetted into individual wells of a 24 well plate to allow collagen gel polymerization. Test agents are added after 30 min by pipetting 100 μl of 10-fold concentrated working dilution of the test substances on top of the gel. Plates are incubated at 37°C for 24h. Dishes are fixed at the end of the experimental incubation period by addition of paraformaldehyde. Sprouting intensity of endothelial cells can be quantitated by an automated image analysis system to determine the cumulative sprout length per spheroid.

Primary assays for antibody modulators

For antibody modulators, appropriate primary assays test is a binding assay that tests the antibody's affinity to and specificity for the MBCAT protein. Methods for testing antibody affinity and specificity are well known in the art (Harlow and Lane, 1988, 1999, *supra*). The enzyme-linked immunosorbant assay (ELISA) is a preferred method for detecting MBCAT-specific antibodies; others include FACS assays, radioimmunoassays, and fluorescent assays.

In some cases, screening assays described for small molecule modulators may also be used to test antibody modulators.

Primary assays for nucleic acid modulators

For nucleic acid modulators, primary assays may test the ability of the nucleic acid modulator to inhibit or enhance MBCAT gene expression, preferably mRNA expression. In general, expression analysis comprises comparing MBCAT expression in like populations of cells (*e.g.*, two pools of cells that endogenously or recombinantly express MBCAT) in the presence and absence of the nucleic acid modulator. Methods for analyzing mRNA and protein expression are well known in the art. For instance, Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR (*e.g.*, using the TaqMan®, PE Applied Biosystems), or microarray analysis may be used to confirm that MBCAT mRNA expression is reduced in cells treated with the nucleic acid modulator (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, *eds.*, John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 33:142-147; Blohm DH and Guiseppi-Elie, A Curr Opin Biotechnol 2001, 12:41-47). Protein expression may also be monitored. Proteins are most commonly detected with specific antibodies or antisera directed against either the MBCAT protein or specific peptides. A variety of means including Western blotting, ELISA, or in situ detection, are available (Harlow E and Lane D, 1988 and 1999, *supra*).

In some cases, screening assays described for small molecule modulators, particularly in assay systems that involve MBCAT mRNA expression, may also be used to test nucleic acid modulators.

Secondary Assays

Secondary assays may be used to further assess the activity of MBCAT-modulating agent identified by any of the above methods to confirm that the modulating agent affects MBCAT in a manner relevant to the beta-catenin pathway. As used herein, MBCAT-modulating agents encompass candidate clinical compounds or other agents derived from previously identified modulating agent. Secondary assays can also be used to test the activity of a modulating agent on a particular genetic or biochemical pathway or to test the specificity of the modulating agent's interaction with MBCAT.

Secondary assays generally compare like populations of cells or animals (*e.g.*, two pools of cells or animals that endogenously or recombinantly express MBCAT) in the presence and absence of the candidate modulator. In general, such assays test whether treatment of cells or animals with a candidate MBCAT–modulating agent results in changes in the beta-catenin pathway in comparison to untreated (or mock- or placebo-

treated) cells or animals. Certain assays use "sensitized genetic backgrounds", which, as used herein, describe cells or animals engineered for altered expression of genes in the beta-catenin or interacting pathways.

Cell-based assays

Cell based assays may detect endogenous beta-catenin pathway activity or may rely on recombinant expression of beta-catenin pathway components. Any of the aforementioned assays may be used in this cell-based format. Candidate modulators are typically added to the cell media but may also be injected into cells or delivered by any other efficacious means.

Animal Assays

A variety of non-human animal models of normal or defective beta-catenin pathway may be used to test candidate MBCAT modulators. Models for defective beta-catenin pathway typically use genetically modified animals that have been engineered to mis-express (*e.g.*, over-express or lack expression in) genes involved in the beta-catenin pathway. Assays generally require systemic delivery of the candidate modulators, such as by oral administration, injection, etc.

In a preferred embodiment, beta-catenin pathway activity is assessed by monitoring neovascularization and angiogenesis. Animal models with defective and normal beta-catenin are used to test the candidate modulator's affect on MBCAT in Matrigel® assays. Matrigel® is an extract of basement membrane proteins, and is composed primarily of laminin, collagen IV, and heparin sulfate proteoglycan. It is provided as a sterile liquid at 4° C, but rapidly forms a solid gel at 37° C. Liquid Matrigel® is mixed with various angiogenic agents, such as bFGF and VEGF, or with human tumor cells which over-express the MBCAT. The mixture is then injected subcutaneously(SC) into female athymic nude mice (Taconic, Germantown, NY) to support an intense vascular response. Mice with Matrigel® pellets may be dosed via oral (PO), intraperitoneal (IP), or intravenous (IV) routes with the candidate modulator. Mice are euthanized 5 - 12 days post-injection, and the Matrigel® pellet is harvested for hemoglobin analysis (Sigma plasma hemoglobin kit). Hemoglobin content of the gel is found to correlate the degree of neovascularization in the gel.

In another preferred embodiment, the effect of the candidate modulator on MBCAT is assessed via tumorigenicity assays. Tumor xenograft assays are known in the

art (see, e.g., Ogawa K et al., 2000, Oncogene 19:6043-6052). Xenografts are typically implanted SC into female athymic mice, 6-7 week old, as single cell suspensions either from a pre-existing tumor or from *in vitro* culture. The tumors which express the MBCAT endogenously are injected in the flank, 1 x 10^5 to 1 x 10^7 cells per mouse in a volume of 100 µL using a 27gauge needle. Mice are then ear tagged and tumors are measured twice weekly. Candidate modulator treatment is initiated on the day the mean tumor weight reaches 100 mg. Candidate modulator is delivered IV, SC, IP, or PO by bolus administration. Depending upon the pharmacokinetics of each unique candidate modulator, dosing can be performed multiple times per day. The tumor weight is assessed by measuring perpendicular diameters with a caliper and calculated by multiplying the measurements of diameters in two dimensions. At the end of the experiment, the excised tumors maybe utilized for biomarker identification or further analyses. For immunohistochemistry staining, xenograft tumors are fixed in 4% paraformaldehyde, 0.1M phosphate, pH 7.2, for 6 hours at 4°C, immersed in 30% sucrose in PBS, and rapidly frozen in isopentane cooled with liquid nitrogen.

In another preferred embodiment, tumorogenicity is monitored using a hollow fiber assay, which is described in U.S. Pat No. US 5,698,413. Briefly, the method comprises implanting into a laboratory animal a biocompatible, semi-permeable encapsulation device containing target cells, treating the laboratory animal with a candidate modulating agent, and evaluating the target cells for reaction to the candidate modulator. Implanted cells are generally human cells from a pre-existing tumor or a tumor cell line. After an appropriate period of time, generally around six days, the implanted samples are harvested for evaluation of the candidate modulator. Tumorogenicity and modulator efficacy may be evaluated by assaying the quantity of viable cells present in the macrocapsule, which can be determined by tests known in the art, for example, MTT dye conversion assay, neutral red dye uptake, trypan blue staining, viable cell counts, the number of colonies formed in soft agar, the capacity of the cells to recover and replicate in vitro, etc.

In another preferred embodiment, a tumorogenicity assay use a transgenic animal, usually a mouse, carrying a dominant oncogene or tumor suppressor gene knockout under the control of tissue specific regulatory sequences; these assays are generally referred to as transgenic tumor assays. In a preferred application, tumor development in the transgenic model is well characterized or is controlled. In an exemplary model, the "RIP1-Tag2" transgene, comprising the SV40 large T-antigen oncogene under control of the insulin gene regulatory regions is expressed in pancreatic beta cells and results in islet cell

carcinomas (Hanahan D, 1985, Nature 315:115-122; Parangi S et al, 1996, Proc Natl Acad Sci USA 93: 2002-2007; Bergers G et al, 1999, Science 284:808-812). An "angiogenic switch," occurs at approximately five weeks, as normally quiescent capillaries in a subset of hyperproliferative islets become angiogenic. The RIP1-TAG2 mice die by age 14 weeks. Candidate modulators may be administered at a variety of stages, including just prior to the angiogenic switch (e.g., for a model of tumor prevention), during the growth of small tumors (e.g., for a model of intervention), or during the growth of large and/or invasive tumors (e.g., for a model of regression). Tumorogenicity and modulator efficacy can be evaluating life-span extension and/or tumor characteristics, including number of tumors, tumor size, tumor morphology, vessel density, apoptotic index, etc.

Diagnostic and therapeutic uses

Specific MBCAT-modulating agents are useful in a variety of diagnostic and therapeutic applications where disease or disease prognosis is related to defects in the beta-catenin pathway, such as angiogenic, apoptotic, or cell proliferation disorders. Accordingly, the invention also provides methods for modulating the beta-catenin pathway in a cell, preferably a cell pre-determined to have defective or impaired beta-catenin function (e.g. due to overexpression, underexpression, or misexpression of beta-catenin, or due to gene mutations), comprising the step of administering an agent to the cell that specifically modulates MBCAT activity. Preferably, the modulating agent produces a detectable phenotypic change in the cell indicating that the beta-catenin function is restored. The phrase "function is restored", and equivalents, as used herein, means that the desired phenotype is achieved, or is brought closer to normal compared to untreated cells. For example, with restored beta-catenin function, cell proliferation and/or progression through cell cycle may normalize, or be brought closer to normal relative to untreated cells. The invention also provides methods for treating disorders or disease associated with impaired beta-catenin function by administering a therapeutically effective amount of an MBCAT -modulating agent that modulates the beta-catenin pathway. The invention further provides methods for modulating MBCAT function in a cell, preferably a cell pre-determined to have defective or impaired MBCAT function, by administering an MBCAT -modulating agent. Additionally, the invention provides a method for treating disorders or disease associated with impaired MBCAT function by administering a therapeutically effective amount of an MBCAT -modulating agent.

The discovery that MBCAT is implicated in beta-catenin pathway provides for a variety of methods that can be employed for the diagnostic and prognostic evaluation of diseases and disorders involving defects in the beta-catenin pathway and for the identification of subjects having a predisposition to such diseases and disorders.

Various expression analysis methods can be used to diagnose whether MBCAT expression occurs in a particular sample, including Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR, and microarray analysis. (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, *eds.*, John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 33:142-147; Blohm and Guiseppi-Elie, Curr Opin Biotechnol 2001, 12:41-47). Tissues having a disease or disorder implicating defective beta-catenin signaling that express an MBCAT, are identified as amenable to treatment with an MBCAT modulating agent. In a preferred application, the beta-catenin defective tissue overexpresses an MBCAT relative to normal tissue. For example, a Northern blot analysis of mRNA from tumor and normal cell lines, or from tumor and matching normal tissue samples from the same patient, using full or partial MBCAT cDNA sequences as probes, can determine whether particular tumors express or overexpress MBCAT. Alternatively, the TaqMan® is used for quantitative RT-PCR analysis of MBCAT expression in cell lines, normal tissues and tumor samples (PE Applied Biosystems).

Various other diagnostic methods may be performed, for example, utilizing reagents such as the MBCAT oligonucleotides, and antibodies directed against an MBCAT, as described above for: (1) the detection of the presence of MBCAT gene mutations, or the detection of either over- or under-expression of MBCAT mRNA relative to the non-disorder state; (2) the detection of either an over- or an under-abundance of MBCAT gene product relative to the non-disorder state; and (3) the detection of perturbations or abnormalities in the signal transduction pathway mediated by MBCAT.

Thus, in a specific embodiment, the invention is drawn to a method for diagnosing a disease or disorder in a patient that is associated with alterations in MBCAT expression, the method comprising: a) obtaining a biological sample from the patient; b) contacting the sample with a probe for MBCAT expression; c) comparing results from step (b) with a control; and d) determining whether step (c) indicates a likelihood of the disease or disorder. Preferably, the disease is cancer, most preferably a cancer as shown in TABLE 2. The probe may be either DNA or protein, including an antibody.

EXAMPLES

The following experimental section and examples are offered by way of illustration and not by way of limitation.

I. C. elegans beta-catenin screen

The identification of mutants that suppress the cell adhesion defect of beta-catenin may lead to unique therapeutic targets that inhibit cell migration or metastasis. *hmp-2* was initially identified in an EMS screen for defects in body elongation during embryonic morphogenesis (see Costa *et al.*, (1998) The Journal of Cell Biology 1998, 141: 297-308). The loss of function allele *hmp-2 (zu364)* exhibits 99% embryonic lethality, with mutant embryos arresting during elongation and abnormal bulges forming on the dorsal side. About 1% of these embryos hatch to form viable lumpy larvae. The reduction of function allele *hmp-2 (qm39)* yields viable larvae with a characteristic lumpy appearance. When grown at 15°C, approximately 92% (SD 3.9) of the L1 larvae show this lumpy phenotype, with the penetrance of the phenotype decreasing as the animals molt and move through successive larval stages. For this screen, *hmp-2 (qm39)* worms were soaked at 15°C in double stranded RNA (dsRNA) at the L4 larval stage and the progeny were scored as L1 larvae for modification of the adhesion defect. The screen protocol is described below.

1) *hmp-2 (qm39)* animals were bleached and hatched on peptone free agarose plates to produce a synchronous population. Starved L1s were transferred to 10x peptone plates seeded with 750 µl OP50 (25% w/v in TB) and allowed to develop to the L4 larval stage.

2) dsRNA was dispensed in 6 µl aliquots into 96 well round bottom plates (Nunc #262162). L4 animals were collected by suspension in M9 buffer, washed 2x with M9 to remove any excess OP50, and dispensed in 2 µl aliquots into the RNA to a total worm density of 75-100 worms per well. As a control, multiple wells contained only RNA resuspension buffer (1x IM buffer).

3) Animals were soaked in dsRNA at 15°C for 24 hours.

4) Following dsRNA soaking, the animals were fed in the wells by addition of 25µl liquid NGM + 3% OP50. The animals were kept at 15°C and allowed to become gravid and lay progeny in the wells, which took approximately 72 hours. Food levels were monitored visually during maturation and more was added as needed.

5) Following maturation, animals from each well were plated onto individual 6cm peptone free agarose plates and placed at 15°C overnight.

6) Animals on each plate were scored visually under the dissecting microscope for modification of the lumpy phenotype. Scoring was performed qualitatively, with an increase in dead embryos scored as enhancement and an increase in wild type appearing animals scored as suppression of the defect.

7) Retests of interesting suppressor candidates followed the same protocol as the primary screen with certain modifications: several retests were performed for each suppressor, retested candidates were encoded so that they could be scored blindly, and retested candidates were scored quantitatively. Each plate was scored by counting 100 total objects. An object was defined as either an embryo or an L1 stage larva. Each object was scored as one of the following: a wildtype appearing animal, a lumpy appearing animal, or an unhatched embryo. Scores were represented as the percentage of wildtype appearing animals relative to all objects scored. Wildtype animals were defined as L1 larvae with smooth cuticles that did not have any sort of lumpy body morphology.

8) A confirmed suppressor was one that was ≥ 2 standard deviations away from the mean of the controls for at least 3 of the four retest experiments.

II. Analysis of Table 1

BLAST analysis (Altschul et al., *supra*) was employed to identify Targets from *C. elegans* modifiers. The columns "MBCAT symbol", and "MBCAT name aliases " provide a symbol and the known name abbreviations for the Targets, where available, from Genbank. "MBCAT RefSeq_NA or GI_NA", "MBCAT GI_AA", "MBCAT NAME", and "MBCAT Description" provide the reference DNA sequences for the MBCATs as available from National Center for Biology Information (NCBI), MBCAT protein Genbank identifier number (GI#), MBCAT name, and MBCAT description, all available from Genbank, respectively. The length of each amino acid is in the "MBCAT Protein Length" column.

Names and Protein sequences of *C. elegans* modifiers of beta-catenin from screen (Example I), are represented in the "Modifier Name" and "Modifier GI_AA" column by GI#, respectively.

TABLE1

BCAT symbol	MBCAT name aliases	MBCAT RefSeq_NA or GI_NA	NASEQ ID NO	MBCAT GI_AA or RefSeq_AA	AA SEQ ID NO	MBCAT name	MBCAT description	MBCAT protein length	Modifier name	Modifier GI_AA
DLG1	hdlg, SAP97	NM_004087	1	4758162 NP_004078.1	10	gi|4758162|ref|NP_004078.1| discs, large (Drosophila) homolog 1 [Homo sapiens]	Homolog of Drosophila discs large tumor suppressor 1; putative kinase, binds EPB41, may have structural and signaling roles; member of the membrane-associated guanylate kinase (MAGUK) family	926aa	C25F6.2	13775380
DLG2	PSD-93, chapsyn-110	NM_001364	2	4557527 NP_001355.1	11	gi|4557527|ref|NP_001355.1| discs, large (Drosophila) homolog 2 [Homo sapiens]	DLG2 is a member of the membrane-associated guanylate kinase (MAGUK) family. It heteromultimerizes with DLG4. With DLG4 it is recruited into the same NMDA receptor and potassium channel clusters. These 2 MAGUK proteins may interact at postsynaptic sites to form a multimeric scaffold for the clustering of receptors, ion channels, and associated signaling proteins. Chapsyn-110; may mediate organized clustering of NMDA receptors and Shaker-family K+ channel subunits in nerve cells; strongly similar to rat Chapsyn-110	870aa	C25F6.2	13775380

DLG3	NEDLG, NE-DLG, NE-dlg, SAP102	NM_021120	3	10863921 NP_066943.1	12	gi|10863921|ref|NP_066943.1| discs, large (Drosophila) homolog 3 [Homo sapiens]	NA	817aa	C25F6.2	13775380
DLG4	PSD95, SAP90, PSD-95	NM_001365	4	4557529 NP_001356.1	13	gi|4557529|ref|NP_001356.1| discs, large (Drosophila) homolog 4 [Homo sapiens]	DLG4 is a member of the membrane-associated guanylate kinase (MAGUK) family. It heteromultimerizes with DLG2. With DLG2 it is recruited into the same NMDA receptor and potassium channel clusters. These 2 MAGUK proteins may interact at postsynaptic sites to form a multimeric scaffold for the clustering of receptors, ion channels, and associated signaling proteins.	767aa	C25F6.2	13775380
LOC89363	DLG3	XM_034696	5	14786086 XP_034696.1	14	gi|14786086|ref|XP_034696.1| KIAA1232 protein [Homo sapiens]	NA	512aa	C25F6.2	13775380
HSPC111	HSPC185, CGI-117	NM_016391	6	7705451 NP_057475.1	15	gi|7705451|ref|NP_057475.1| hypothetical protein; CGI-117 protein [Homo sapiens]	NA	178aa	ZK265.6	17511059
LOC55974	SCP	NM_018845; 6563277; 16307087	7, 8, 9	10047124 NP_061333.1	16	gi|10047124|ref|NP_061333.1| stromal cell protein [Homo sapiens]	Highly similar to murine Rga; may be a membrane receptor	221aa	K02D7.5	17541198

III. High-Throughput In Vitro Fluorescence Polarization Assay

Fluorescently-labeled MBCAT peptide/substrate are added to each well of a 96-well microtiter plate, along with a test agent in a test buffer (10 mM HEPES, 10 mM

NaCl, 6 mM magnesium chloride, pH 7.6). Changes in fluorescence polarization, determined by using a Fluorolite FPM-2 Fluorescence Polarization Microtiter System (Dynatech Laboratories, Inc), relative to control values indicates the test compound is a candidate modifier of MBCAT activity.

IV. High-Throughput In Vitro Binding Assay.

^{33}P-labeled MBCAT peptide is added in an assay buffer (100 mM KCl, 20 mM HEPES pH 7.6, 1 mM $MgCl_2$, 1% glycerol, 0.5% NP-40, 50 mM beta-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors) along with a test agent to the wells of a Neutralite-avidin coated assay plate and incubated at 25°C for 1 hour. Biotinylated substrate is then added to each well and incubated for 1 hour. Reactions are stopped by washing with PBS, and counted in a scintillation counter. Test agents that cause a difference in activity relative to control without test agent are identified as candidate beta-catenin modulating agents.

V. Immunoprecipitations and Immunoblotting

For coprecipitation of transfected proteins, 3×10^6 appropriate recombinant cells containing the MBCAT proteins are plated on 10-cm dishes and transfected on the following day with expression constructs. The total amount of DNA is kept constant in each transfection by adding empty vector. After 24 h, cells are collected, washed once with phosphate-buffered saline and lysed for 20 min on ice in 1 ml of lysis buffer containing 50 mM Hepes, pH 7.9, 250 mM NaCl, 20 mM -glycerophosphate, 1 mM sodium orthovanadate, 5 mM p-nitrophenyl phosphate, 2 mM dithiothreitol, protease inhibitors (complete, Roche Molecular Biochemicals), and 1% Nonidet P-40. Cellular debris is removed by centrifugation twice at 15,000 × g for 15 min. The cell lysate is incubated with 25 μl of M2 beads (Sigma) for 2 h at 4 °C with gentle rocking.

After extensive washing with lysis buffer, proteins bound to the beads are solubilized by boiling in SDS sample buffer, fractionated by SDS-polyacrylamide gel electrophoresis, transferred to polyvinylidene difluoride membrane and blotted with the indicated antibodies. The reactive bands are visualized with horseradish peroxidase coupled to the appropriate secondary antibodies and the enhanced chemiluminescence (ECL) Western blotting detection system (Amersham Pharmacia Biotech).

VI. Kinase assay

A purified or partially purified MBCAT is diluted in a suitable reaction buffer, e.g., 50 mM Hepes, pH 7.5, containing magnesium chloride or manganese chloride (1-20 mM) and a peptide or polypeptide substrate, such as myelin basic protein or casein (1-10 μg/ml). The final concentration of the kinase is 1-20 nM. The enzyme reaction is conducted in microtiter plates to facilitate optimization of reaction conditions by increasing assay throughput. A 96-well microtiter plate is employed using a final volume 30-100 μl. The reaction is initiated by the addition of ^{33}P-gamma-ATP (0.5 μCi/ml) and incubated for 0.5 to 3 hours at room temperature. Negative controls are provided by the addition of EDTA, which chelates the divalent cation ($Mg2^+$ or Mn^{2+}) required for enzymatic activity. Following the incubation, the enzyme reaction is quenched using EDTA. Samples of the reaction are transferred to a 96-well glass fiber filter plate (MultiScreen, Millipore). The filters are subsequently washed with phosphate-buffered saline, dilute phosphoric acid (0.5%) or other suitable medium to remove excess radiolabeled ATP. Scintillation cocktail is added to the filter plate and the incorporated radioactivity is quantitated by scintillation counting (Wallac/Perkin Elmer). Activity is defined by the amount of radioactivity detected following subtraction of the negative control reaction value (EDTA quench).

VII. Expression analysis

All cell lines used in the following experiments are NCI (National Cancer Institute) lines, and are available from ATCC (American Type Culture Collection, Manassas, VA 20110-2209). Normal and tumor tissues were obtained from Impath, UC Davis, Clontech, Stratagene, Ardais, Genome Collaborative, and Ambion.

TaqMan analysis was used to assess expression levels of the disclosed genes in various samples.

RNA was extracted from each tissue sample using Qiagen (Valencia, CA) RNeasy kits, following manufacturer's protocols, to a final concentration of 50ng/μl. Single stranded cDNA was then synthesized by reverse transcribing the RNA samples using random hexamers and 500ng of total RNA per reaction, following protocol 4304965 of Applied Biosystems (Foster City, CA).

Primers for expression analysis using TaqMan assay (Applied Biosystems, Foster City, CA) were prepared according to the TaqMan protocols, and the following criteria: a) primer pairs were designed to span introns to eliminate genomic contamination, and b)

each primer pair produced only one product. Expression analysis was performed using a 7900HT instrument.

Taqman reactions were carried out following manufacturer's protocols, in 25 µl total volume for 96-well plates and 10 µl total volume for 384-well plates, using 300nM primer and 250 nM probe, and approximately 25ng of cDNA. The standard curve for result analysis was prepared using a universal pool of human cDNA samples, which is a mixture of cDNAs from a wide variety of tissues so that the chance that a target will be present in appreciable amounts is good. The raw data were normalized using 18S rRNA (universally expressed in all tissues and cells).

For each expression analysis, tumor tissue samples were compared with matched normal tissues from the same patient. A gene was considered overexpressed in a tumor when the level of expression of the gene was 2 fold or higher in the tumor compared with its matched normal sample. In cases where normal tissue was not available, a universal pool of cDNA samples was used instead. In these cases, a gene was considered overexpressed in a tumor sample when the difference of expression levels between a tumor sample and the average of all normal samples from the same tissue type was greater than 2 times the standard deviation of all normal samples (i.e., Tumor – average(all normal samples) > 2 x STDEV(all normal samples)).

Results are shown in Table 2. Number of pairs of tumor samples and matched normal tissue from the same patient are shown for each tumor type. Percentage of the samples with at least two-fold overexpression for each tumor type is provided. A modulator identified by an assay described herein can be further validated for therapeutic effect by administration to a tumor in which the gene is overexpressed. A decrease in tumor growth confirms therapeutic utility of the modulator. Prior to treating a patient with the modulator, the likelihood that the patient will respond to treatment can be diagnosed by obtaining a tumor sample from the patient, and assaying for expression of the gene targeted by the modulator. The expression data for the gene(s) can also be used as a diagnostic marker for disease progression. The assay can be performed by expression analysis as described above, by antibody directed to the gene target, or by any other available detection method.

Table 2

GI#	SEQ ID NO:	Breast	# of Pairs	Colon	# of Pairs	Head and Neck	# of Pairs	Kidney	# of Pairs	Lung	# of Pairs	Ovary	# of Pairs	Uterus	# of Pairs	Prostate	# of Pairs	Skin	# of Pairs
7705450	6	21%	19	48%	33	13%	8	17%	24	35%	20	55%	11	16%	19	17%	12	67%	3
16307087	9	53%	19	45%	33	50%	8	33%	24	57%	21	83%	12	26%	19	8%	12	67%	3

WHAT IS CLAIMED IS:

1. A method of identifying a candidate beta-catenin pathway modulating agent, said method comprising the steps of:

(a) providing an assay system comprising a MBCAT polypeptide or nucleic acid;

(b) contacting the assay system with a test agent under conditions whereby, but for the presence of the test agent, the system provides a reference activity; and

(c) detecting a test agent-biased activity of the assay system, wherein a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate beta-catenin pathway modulating agent.

2. The method of Claim 1 wherein the assay system comprises cultured cells that express the MBCAT polypeptide.

3. The method of Claim 2 wherein the cultured cells additionally have defective beta-catenin function.

4. The method of Claim 1 wherein the assay system includes a screening assay comprising a MBCAT polypeptide, and the candidate test agent is a small molecule modulator.

5. The method of Claim 4 wherein the assay is a binding assay.

6. The method of Claim 1 wherein the assay system is selected from the group consisting of an apoptosis assay system, a cell proliferation assay system, an angiogenesis assay system, and a hypoxic induction assay system.

7. The method of Claim 1 wherein the assay system includes a binding assay comprising a MBCAT polypeptide and the candidate test agent is an antibody.

8. The method of Claim 1 wherein the assay system includes an expression assay comprising a MBCAT nucleic acid and the candidate test agent is a nucleic acid modulator.

9. The method of claim 8 wherein the nucleic acid modulator is an antisense oligomer.

10. The method of Claim 8 wherein the nucleic acid modulator is a PMO.

11. The method of Claim 1 additionally comprising:

(d) administering the candidate beta-catenin pathway modulating agent identified in (c) to a model system comprising cells defective in beta-catenin function and, detecting a phenotypic change in the model system that indicates that the beta-catenin function is restored.

12. The method of Claim 11 wherein the model system is a mouse model with defective beta-catenin function.

13. A method for modulating a beta-catenin pathway of a cell comprising contacting a cell defective in beta-catenin function with a candidate modulator that specifically binds to a MBCAT polypeptide comprising an amino acid sequence selected from group consisting of SEQ ID NOs:10, 11, 12, 13, 14, 15, and 16, whereby beta-catenin function is restored.

14. The method of claim 13 wherein the candidate modulator is administered to a vertebrate animal predetermined to have a disease or disorder resulting from a defect in beta-catenin function.

15. The method of Claim 13 wherein the candidate modulator is selected from the group consisting of an antibody and a small molecule.

16. The method of Claim 1, comprising the additional steps of:

(d) providing a secondary assay system comprising cultured cells or a non-human animal expressing MBCAT ,

(e) contacting the secondary assay system with the test agent of (b) or an agent derived therefrom under conditions whereby, but for the presence of the test agent or agent derived therefrom, the system provides a reference activity; and

(f) detecting an agent-biased activity of the second assay system,

wherein a difference between the agent-biased activity and the reference activity of the second assay system confirms the test agent or agent derived therefrom as a candidate beta-catenin pathway modulating agent,

and wherein the second assay detects an agent-biased change in the beta-catenin pathway.

17. The method of Claim 16 wherein the secondary assay system comprises cultured cells.

18. The method of Claim 16 wherein the secondary assay system comprises a non-human animal.

19. The method of Claim 18 wherein the non-human animal mis-expresses a beta-catenin pathway gene.

20. A method of modulating beta-catenin pathway in a mammalian cell comprising contacting the cell with an agent that specifically binds a MBCAT polypeptide or nucleic acid.

21. The method of Claim 20 wherein the agent is administered to a mammalian animal predetermined to have a pathology associated with the beta-catenin pathway.

22. The method of Claim 20 wherein the agent is a small molecule modulator, a nucleic acid modulator, or an antibody.

23. A method for diagnosing a disease in a patient comprising:

(a) obtaining a biological sample from the patient;

(b) contacting the sample with a probe for MBCAT expression;

(c) comparing results from step (b) with a control;

(d) determining whether step (c) indicates a likelihood of disease.

24. The method of claim 23 wherein said disease is cancer.

25. The method according to claim 24, wherein said cancer is a cancer as shown in Table 2 as having >25% expression level.

SEQUENCE LISTING

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ctgagatcgt gccattgtga tatgaatatg ccttatatgc tgatatgaat atgccttaaa 1140

ataaagtgtt ccccacccct gaaaaaaaaa aaaaaaaaaa aaa 1183

<210> 9
<211> 1186
<212> DNA
<213> Homo sapiens

<400> 9
gtaggtcccg gcaaccgcag gctcgcggcg ggcgctgggc gcgggatccg actctagtcg 60

taatggaggc gggcggcttt ctggactcgc tcatttacgg agcatgcgtg gtcttcaccc 120

ttggcatgtt ctccgccggc ctctcggacc tcaggcacat gcgaatgacc cggagtgtgg 180

acaacgtcca gttcctgccc tttctcacca cggaagtcaa caacctgggc tggctgagtt 240

atggggcttt gaagggagac gggatcctca tcgtcgtcaa cacagtgggt gctgcgcttc 300

agaccctgta tatcttggca tatctgcatt actgccctcg gaaggctaag gtgattcaaa 360

ctaaatcaac ccaatgtctc tcctacccac tcaccattgc tacccttctc acctctgcct 420

cctggtgcct ctatgggttt cgactcagag atccctatat catggtgtcc aactttccag 480

gaatcgtcac cagctttatc cgcttctggc ttttctggaa gtacccccag gagcaagaca 540

ggaactactg gctcctgcaa acctgaggct gctcatctga ccactgggca ccttagtgcc 600

aacctgaacc aaagagacct ccttgtttca gctgggcctg ctgtccagct tcccaggtgc 660

agtgggttgt gggaacaaga gatgactttg aggataaaag gaccaaagaa aaagctttac 720

ttagatgatt gattggggcc taggagatga aatcactttt tatttttag agatttttt 780

ttttaatttt ggaggttggg gtgcaatctt tagaatatgc cttaaaaggc cgggcgcggt 840

ggctcacgcc tgtaatccca gcactttggg aggccaaggt gggcggatcg cctgaggtca 900

ggagttcaag accaacctga ctaacatggt gaaaccccat ctctactaaa aatacaaaat 960

tagccaggca tgatggcaca tgcctgtaat cccagatact tgggaggctg aggcaggaga 1020

attgcttgaa cccaggaggt ggaggttgca gtgagctgag atcgtgccat tgtgatatga 1080

atatgcctta tatgctgata tgaatatgcc ttaaaataaa gtgttcccca cccctgcaaa 1140

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1186

<210> 10
<211> 926
<212> PRT
<213> Homo sapiens

<400> 10

Met Pro Val Arg Lys Gln Asp Thr Gln Arg Ala Leu His Leu Leu Glu
1 5 10 15

Glu Tyr Arg Ser Lys Leu Ser Gln Thr Glu Asp Arg Gln Leu Arg Ser
20 25 30

Ser Ile Glu Arg Val Ile Asn Ile Phe Gln Ser Asn Leu Phe Gln Ala
35 40 45

Leu Ile Asp Ile Gln Glu Phe Tyr Glu Val Thr Leu Leu Asp Asn Pro
50 55 60

Lys Cys Ile Asp Arg Ser Lys Pro Ser Glu Pro Ile Gln Pro Val Asn
65 70 75 80

Thr Trp Glu Ile Ser Ser Leu Pro Ser Ser Thr Val Thr Ser Glu Thr
85 90 95

Leu Pro Ser Ser Leu Ser Pro Ser Val Glu Lys Tyr Arg Tyr Gln Asp
100 105 110

Glu Asp Thr Pro Pro Gln Glu His Ile Ser Pro Gln Ile Thr Asn Glu
115 120 125

Val Ile Gly Pro Glu Leu Val His Val Ser Glu Lys Asn Leu Ser Glu
130 135 140

Ile Glu Asn Val His Gly Phe Val Ser His Ser His Ile Ser Pro Ile
145 150 155 160

Lys Pro Thr Glu Ala Val Leu Pro Ser Pro Pro Thr Val Pro Val Ile
165 170 175

Pro Val Leu Pro Val Pro Ala Glu Asn Thr Val Ile Leu Pro Thr Ile
180 185 190

Pro Gln Ala Asn Pro Pro Pro Val Leu Val Asn Thr Asp Ser Leu Glu
195 200 205

Thr Pro Thr Tyr Val Asn Gly Thr Asp Ala Asp Tyr Glu Tyr Glu Glu
210 215 220

Ile Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly
225 230 235 240

Gly Thr Asp Asn Pro His Ile Gly Asp Asp Ser Ser Ile Phe Ile Thr
245 250 255

Lys Ile Ile Thr Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg Val

260 265 270

Asn Asp Cys Ile Leu Gln Val Asn Glu Val Asp Val Arg Asp Val Thr
275 280 285

His Ser Lys Ala Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg
290 295 300

Leu Tyr Val Lys Arg Arg Lys Pro Val Ser Glu Lys Ile Met Glu Ile
305 310 315 320

Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly
325 330 335

Val Gly Asn Gln His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys
340 345 350

Ile Ile Glu Gly Gly Ala Ala His Lys Asp Gly Lys Leu Gln Ile Gly
355 360 365

Asp Lys Leu Leu Ala Val Asn Asn Val Cys Leu Glu Glu Val Thr His
370 375 380

Glu Glu Ala Val Thr Ala Leu Lys Asn Thr Ser Asp Phe Val Tyr Leu
385 390 395 400

Lys Val Ala Lys Pro Thr Ser Met Tyr Met Asn Asp Gly Tyr Ala Pro
405 410 415

Pro Asp Ile Thr Asn Ser Ser Ser Gln Pro Val Asp Asn His Val Ser
420 425 430

Pro Ser Ser Phe Leu Gly Gln Thr Pro Ala Ser Pro Ala Arg Tyr Ser
435 440 445

Pro Val Ser Lys Ala Val Leu Gly Asp Asp Glu Ile Thr Arg Glu Pro
450 455 460

Arg Lys Val Val Leu His Arg Gly Ser Thr Gly Leu Gly Phe Asn Ile
465 470 475 480

Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile Leu Ala
485 490 495

Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp Arg Ile
500 505 510

Ile Ser Val Asn Ser Val Asp Leu Arg Ala Ala Ser His Glu Gln Ala
515 520 525

Ala Ala Ala Leu Lys Asn Ala Gly Gln Ala Val Thr Ile Val Ala Gln
530 535 540

Tyr Arg Pro Glu Glu Tyr Ser Arg Phe Glu Ala Lys Ile His Asp Leu
545 550 555 560

Arg Glu Gln Met Met Asn Ser Ser Ile Ser Ser Gly Ser Gly Ser Leu
565 570 575

Arg Thr Ser Gln Lys Arg Ser Leu Tyr Val Arg Ala Leu Phe Asp Tyr
580 585 590

Asp Lys Thr Lys Asp Ser Gly Leu Pro Ser Gln Gly Leu Asn Phe Lys
595 600 605

Phe Gly Asp Ile Leu His Val Ile Asn Ala Ser Asp Asp Glu Trp Trp
610 615 620

Gln Ala Arg Gln Val Thr Pro Asp Gly Glu Ser Asp Glu Val Gly Val
625 630 635 640

Ile Pro Ser Lys Arg Arg Val Glu Lys Lys Glu Arg Ala Arg Leu Lys
645 650 655

Thr Val Lys Phe Asn Ser Lys Thr Arg Asp Lys Gly Gln Ser Phe Asn
660 665 670

Asp Lys Arg Lys Lys Asn Leu Phe Ser Arg Lys Phe Pro Phe Tyr Lys
675 680 685

Asn Lys Asp Gln Ser Glu Gln Glu Thr Ser Asp Ala Asp Gln His Val
690 695 700

Thr Ser Asn Ala Ser Asp Ser Glu Ser Ser Tyr Arg Gly Gln Glu Glu
705 710 715 720

Tyr Val Leu Ser Tyr Glu Pro Val Asn Gln Gln Glu Val Asn Tyr Thr
725 730 735

Arg Pro Val Ile Ile Leu Gly Pro Met Lys Asp Arg Ile Asn Asp Asp
740 745 750

Leu Ile Ser Glu Phe Pro Asp Lys Phe Gly Ser Cys Val Pro His Thr

755 760 765

Thr Arg Pro Lys Arg Asp Tyr Glu Val Asp Gly Arg Asp Tyr His Phe
770 775 780

Val Thr Ser Arg Glu Gln Met Glu Lys Asp Ile Gln Glu His Lys Phe
785 790 795 800

Ile Glu Ala Gly Gln Tyr Asn Asn His Leu Tyr Gly Thr Ser Val Gln
805 810 815

Ser Val Arg Glu Val Ala Gly Lys Gly Lys His Cys Ile Leu Asp Val
820 825 830

Ser Gly Asn Ala Ile Lys Arg Leu Gln Ile Ala Gln Leu Tyr Pro Ile
835 840 845

Ser Ile Phe Ile Lys Pro Lys Ser Met Glu Asn Ile Met Glu Met Asn
850 855 860

Lys Arg Leu Thr Glu Glu Gln Ala Arg Lys Thr Phe Glu Arg Ala Met
865 870 875 880

Lys Leu Glu Gln Glu Phe Thr Glu His Phe Thr Ala Ile Val Gln Gly
885 890 895

Asp Thr Leu Glu Asp Ile Tyr Asn Gln Val Lys Gln Ile Ile Glu Glu
900 905 910

Gln Ser Gly Ser Tyr Ile Trp Val Pro Ala Lys Glu Lys Leu
915 920 925

<210> 11
<211> 870
<212> PRT
<213> Homo sapiens

<400> 11

Met Phe Phe Ala Cys Tyr Cys Ala Leu Arg Thr Asn Val Lys Lys Tyr
1 5 10 15

Arg Tyr Gln Asp Glu Asp Ala Pro His Asp His Ser Leu Pro Arg Leu
20 25 30

Thr His Glu Val Arg Gly Pro Glu Leu Val His Val Ser Glu Lys Asn
35 40 45

Leu Ser Gln Ile Glu Asn Val His Gly Tyr Val Leu Gln Ser His Ile
50 55 60

Ser Pro Leu Lys Ala Ser Pro Ala Pro Ile Ile Val Asn Thr Asp Thr
65 70 75 80

Leu Asp Thr Ile Pro Tyr Val Asn Gly Thr Glu Ile Glu Tyr Glu Phe
85 90 95

Glu Glu Ile Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile
100 105 110

Ala Gly Gly Thr Asp Asn Pro His Ile Gly Asp Asp Pro Gly Ile Phe
115 120 125

Ile Thr Lys Ile Ile Pro Gly Gly Ala Ala Ala Glu Asp Gly Arg Leu
130 135 140

Arg Val Asn Asp Cys Ile Leu Arg Val Asn Glu Val Asp Val Ser Glu
145 150 155 160

Val Ser His Ser Lys Ala Val Glu Ala Leu Lys Glu Ala Gly Ser Ile
165 170 175

Ala Arg Leu Tyr Val Arg Arg Arg Arg Pro Ile Leu Glu Thr Val Val
180 185 190

Glu Ile Lys Leu Phe Lys Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala
195 200 205

Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn Ser Ile Tyr Val
210 215 220

Thr Lys Ile Ile Asp Gly Gly Ala Ala Gln Lys Asp Gly Arg Leu Gln
225 230 235 240

Val Gly Asp Arg Leu Leu Met Val Asn Asn Tyr Ser Leu Glu Glu Val
245 250 255

Thr His Glu Glu Ala Val Ala Ile Leu Lys Asn Thr Ser Glu Val Val
260 265 270

Tyr Leu Lys Val Gly Asn Pro Thr Thr Ile Tyr Met Thr Asp Pro Tyr
275 280 285

Gly Pro Pro Asp Ile Thr His Ser Tyr Ser Pro Pro Met Glu Asn His
290 295 300

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Leu Leu Ser Gly Asn Asn Gly Thr Leu Glu Tyr Lys Thr Ser Leu Pro
305                 310                 315                 320

Pro Ile Ser Pro Gly Arg Tyr Ser Pro Ile Pro Lys His Met Leu Val
                325                 330                 335

Asp Asp Asp Tyr Thr Arg Pro Pro Glu Pro Val Tyr Ser Thr Val Asn
            340                 345                 350

Lys Leu Cys Asp Lys Pro Ala Ser Pro Arg His Tyr Ser Pro Val Glu
        355                 360                 365

Cys Asp Lys Ser Phe Leu Leu Ser Ala Pro Tyr Ser His Tyr His Leu
    370                 375                 380

Gly Leu Leu Pro Asp Ser Glu Met Thr Ser His Ser Gln His Ser Thr
385                 390                 395                 400

Ala Thr Arg Gln Pro Ser Met Thr Leu Gln Arg Ala Val Ser Leu Glu
                405                 410                 415

Gly Glu Pro Arg Lys Val Val Leu His Lys Gly Ser Thr Gly Leu Gly
            420                 425                 430

Phe Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Val Ser Phe
        435                 440                 445

Ile Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Gln Arg Gly
    450                 455                 460

Asp Gln Ile Leu Ser Val Asn Gly Ile Asp Leu Arg Gly Ala Ser His
465                 470                 475                 480

Glu Gln Ala Ala Ala Ala Leu Lys Gly Ala Gly Gln Thr Val Thr Ile
                485                 490                 495

Ile Ala Gln Tyr Gln Pro Glu Asp Tyr Ala Arg Phe Glu Ala Lys Ile
            500                 505                 510

His Asp Leu Arg Glu Gln Met Met Asn His Ser Met Ser Ser Gly Ser
        515                 520                 525

Gly Ser Leu Arg Thr Asn Gln Lys Arg Ser Leu Tyr Val Arg Ala Met
    530                 535                 540
```

Phe Asp Tyr Asp Lys Ser Lys Asp Ser Gly Leu Pro Ser Gln Gly Leu
545 550 555 560

Ser Phe Lys Tyr Gly Asp Ile Leu His Val Ile Asn Ala Ser Asp Asp
565 570 575

Glu Trp Trp Gln Ala Arg Arg Val Met Leu Glu Gly Asp Ser Glu Glu
580 585 590

Met Gly Val Ile Pro Ser Lys Arg Arg Val Glu Arg Lys Glu Arg Ala
595 600 605

Arg Leu Lys Thr Val Lys Phe Asn Ala Lys Pro Gly Val Ile Asp Ser
610 615 620

Lys Gly Ser Phe Asn Asp Lys Arg Lys Lys Ser Phe Ile Phe Ser Arg
625 630 635 640

Lys Phe Pro Phe Tyr Lys Asn Lys Glu Gln Ser Glu Gln Glu Thr Ser
645 650 655

Asp Pro Glu Arg Gly Gln Glu Asp Leu Ile Leu Ser Tyr Glu Pro Val
660 665 670

Thr Arg Gln Glu Ile Asn Tyr Thr Arg Pro Val Ile Ile Leu Gly Pro
675 680 685

Met Lys Asp Arg Ile Asn Asp Asp Leu Ile Ser Glu Phe Pro Asp Lys
690 695 700

Phe Gly Ser Cys Val Pro His Thr Thr Arg Pro Lys Arg Asp Tyr Glu
705 710 715 720

Val Asp Gly Arg Asp Tyr His Phe Val Ile Ser Arg Glu Gln Met Glu
725 730 735

Lys Asp Ile Gln Glu His Lys Phe Ile Glu Ala Gly Gln Tyr Asn Asp
740 745 750

Asn Leu Tyr Gly Thr Ser Val Gln Ser Val Arg Phe Val Ala Glu Arg
755 760 765

Gly Lys His Cys Ile Leu Asp Val Ser Gly Asn Ala Ile Lys Arg Leu
770 775 780

Gln Val Ala Gln Leu Tyr Pro Ile Ala Ile Phe Ile Lys Pro Arg Ser
785 790 795 800

Leu Glu Ser Leu Met Glu Met Asn Lys Arg Leu Thr Glu Glu Gln Ala
805 810 815

Lys Lys Thr Tyr Asp Arg Ala Ile Lys Leu Glu Gln Glu Phe Gly Glu
820 825 830

Tyr Phe Thr Ala Ile Val Gln Gly Asp Thr Leu Glu Asp Ile Tyr Asn
835 840 845

Gln Cys Lys Leu Val Ile Glu Glu Gln Ser Gly Pro Phe Ile Trp Ile
850 855 860

Pro Ser Lys Glu Lys Leu
865 870

<210> 12
<211> 817
<212> PRT
<213> Homo sapiens

<400> 12

Met His Lys His Gln His Cys Cys Lys Cys Pro Glu Cys Tyr Glu Val
1 5 10 15

Thr Arg Leu Ala Ala Leu Arg Arg Leu Glu Pro Pro Gly Tyr Gly Asp
20 25 30

Trp Gln Val Pro Asp Pro Tyr Gly Pro Gly Gly Gly Asn Gly Ala Ser
35 40 45

Ala Gly Tyr Gly Gly Tyr Ser Ser Gln Thr Leu Pro Ser Gln Ala Gly
50 55 60

Ala Thr Pro Thr Pro Arg Thr Lys Ala Lys Leu Ile Pro Thr Gly Arg
65 70 75 80

Asp Val Gly Pro Val Pro Leu Lys Pro Val Pro Gly Lys Ser Thr Pro
85 90 95

Lys Leu Asn Gly Ser Gly Pro Ser Trp Trp Pro Glu Cys Thr Cys Thr
100 105 110

Asn Arg Asp Trp Tyr Glu Gln Val Asn Gly Ser Asp Gly Met Phe Lys
115 120 125

Tyr Glu Glu Ile Val Leu Glu Arg Gly Asn Ser Gly Leu Gly Phe Ser

130 135 140

Ile Ala Gly Gly Ile Asp Asn Pro His Val Pro Asp Asp Pro Gly Ile
145 150 155 160

Phe Ile Thr Lys Ile Ile Pro Gly Gly Ala Ala Ala Met Asp Gly Arg
165 170 175

Leu Gly Val Asn Asp Cys Val Leu Arg Val Asn Glu Val Glu Val Ser
180 185 190

Glu Val Val His Ser Arg Ala Val Glu Ala Leu Lys Glu Ala Gly Pro
195 200 205

Val Val Arg Leu Val Val Arg Arg Arg Gln Pro Pro Pro Glu Thr Ile
210 215 220

Met Glu Val Asn Leu Leu Lys Gly Pro Lys Gly Leu Gly Phe Ser Ile
225 230 235 240

Ala Gly Gly Ile Gly Asn Gln His Ile Pro Gly Asp Asn Ser Ile Tyr
245 250 255

Ile Thr Lys Ile Ile Glu Gly Gly Ala Ala Gln Lys Asp Gly Arg Leu
260 265 270

Gln Ile Gly Asp Arg Leu Leu Ala Val Asn Asn Thr Asn Leu Gln Asp
275 280 285

Val Arg His Glu Glu Ala Val Ala Ser Leu Lys Asn Thr Ser Asp Met
290 295 300

Val Tyr Leu Lys Val Ala Lys Pro Gly Ser Leu His Leu Asn Asp Met
305 310 315 320

Tyr Ala Pro Pro Asp Tyr Ala Ser Thr Phe Thr Ala Leu Ala Asp Asn
325 330 335

His Ile Ser His Asn Ser Ser Leu Gly Tyr Leu Gly Ala Val Glu Ser
340 345 350

Lys Val Ser Tyr Pro Ala Pro Pro Gln Val Pro Pro Thr Arg Tyr Ser
355 360 365

Pro Ile Pro Arg His Met Leu Ala Glu Glu Asp Phe Thr Arg Glu Pro
370 375 380

Arg Lys Ile Ile Leu His Lys Gly Ser Thr Gly Leu Gly Phe Asn Ile
385 390 395 400

Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Val Ser Phe Ile Leu Ala
405 410 415

Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Arg Gly Asp Arg Ile
420 425 430

Leu Ser Val Asn Gly Val Asn Leu Arg Asn Ala Thr His Glu Gln Ala
435 440 445

Ala Ala Ala Leu Lys Arg Ala Gly Gln Ser Val Thr Ile Val Ala Gln
450 455 460

Tyr Arg Pro Glu Glu Tyr Ser Arg Phe Glu Ser Lys Ile His Asp Leu
465 470 475 480

Arg Glu Gln Met Met Asn Ser Ser Met Ser Ser Gly Ser Gly Ser Leu
485 490 495

Arg Thr Ser Glu Lys Arg Ser Leu Tyr Val Arg Ala Leu Phe Asp Tyr
500 505 510

Asp Arg Thr Arg Asp Ser Cys Leu Pro Ser Gln Gly Leu Ser Phe Ser
515 520 525

Tyr Gly Asp Ile Leu His Val Ile Asn Ala Ser Asp Asp Glu Trp Trp
530 535 540

Gln Ala Arg Leu Val Thr Pro His Gly Glu Ser Glu Gln Ile Gly Val
545 550 555 560

Ile Pro Ser Lys Lys Arg Val Glu Lys Lys Glu Arg Ala Arg Leu Lys
565 570 575

Thr Val Lys Phe His Ala Arg Thr Gly Met Ile Glu Ser Asn Arg Asp
580 585 590

Phe Pro Gly Leu Ser Asp Asp Tyr Tyr Gly Ala Lys Asn Leu Lys Gly
595 600 605

Gln Glu Asp Ala Ile Leu Ser Tyr Glu Pro Val Thr Arg Gln Glu Ile
610 615 620

His Tyr Ala Arg Pro Val Ile Ile Leu Gly Pro Met Lys Asp Arg Val

625 630 635 640

Asn Asp Asp Leu Ile Ser Glu Phe Pro His Lys Phe Gly Ser Cys Val
645 650 655

Pro His Thr Thr Arg Pro Arg Arg Asp Asn Glu Val Asp Gly Gln Asp
660 665 670

Tyr His Phe Val Val Ser Arg Glu Gln Met Glu Lys Asp Ile Gln Asp
675 680 685

Asn Lys Phe Ile Glu Ala Gly Gln Phe Asn Asp Asn Leu Tyr Gly Thr
690 695 700

Ser Ile Gln Ser Val Arg Ala Val Ala Glu Arg Gly Lys His Cys Ile
705 710 715 720

Leu Asp Val Ser Gly Asn Ala Ile Lys Arg Leu Gln Gln Ala Gln Leu
725 730 735

Tyr Pro Ile Ala Ile Phe Ile Lys Pro Lys Ser Ile Glu Ala Leu Met
740 745 750

Glu Met Asn Arg Arg Gln Thr Tyr Glu Gln Ala Asn Lys Ile Tyr Asp
755 760 765

Lys Ala Met Lys Leu Glu Gln Glu Phe Gly Glu Tyr Phe Thr Ala Ile
770 775 780

Val Gln Gly Asp Ser Leu Glu Glu Ile Tyr Asn Lys Ile Lys Gln Ile
785 790 795 800

Ile Glu Asp Gln Ser Gly His Tyr Ile Trp Val Pro Ser Pro Glu Lys
805 810 815

Leu

<210> 13
<211> 767
<212> PRT
<213> Homo sapiens

<400> 13

Met Ser Gln Arg Pro Arg Ala Pro Arg Ser Ala Leu Trp Leu Leu Ala
1 5 10 15

Pro Pro Leu Leu Arg Trp Ala Pro Pro Leu Leu Thr Val Leu His Ser
20 25 30

Asp Leu Phe Gln Ala Leu Leu Asp Ile Leu Asp Tyr Tyr Glu Ala Ser
35 40 45

Leu Ser Glu Ser Gln Lys Tyr Arg Tyr Gln Asp Glu Asp Thr Pro Pro
50 55 60

Leu Glu His Ser Pro Ala His Leu Pro Asn Gln Ala Asn Ser Pro Pro
65 70 75 80

Val Ile Val Asn Thr Asp Thr Leu Glu Ala Pro Gly Tyr Glu Leu Gln
85 90 95

Val Asn Gly Thr Glu Gly Glu Met Glu Tyr Glu Glu Ile Thr Leu Glu
100 105 110

Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly Gly Thr Asp Asn
115 120 125

Pro His Ile Gly Asp Asp Pro Ser Ile Phe Ile Thr Lys Ile Ile Pro
130 135 140

Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg Val Asn Asp Ser Ile
145 150 155 160

Leu Phe Val Asn Glu Val Asp Val Arg Glu Val Thr His Ser Ala Ala
165 170 175

Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg Leu Tyr Val Met
180 185 190

Arg Arg Lys Pro Pro Ala Glu Lys Val Met Glu Ile Lys Leu Ile Lys
195 200 205

Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly Val Gly Asn Gln
210 215 220

His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly
225 230 235 240

Gly Ala Ala His Lys Asp Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu
245 250 255

Ala Val Asn Ser Val Gly Leu Glu Asp Val Met His Glu Asp Ala Val
260 265 270

Ala Ala Leu Lys Asn Thr Tyr Asp Val Val Tyr Leu Lys Val Ala Lys
275 280 285

Pro Ser Asn Ala Tyr Leu Ser Asp Ser Tyr Ala Pro Pro Asp Ile Thr
290 295 300

Thr Ser Tyr Ser Gln His Leu Asp Asn Glu Ile Ser His Ser Ser Tyr
305 310 315 320

Leu Gly Thr Asp Tyr Pro Thr Ala Met Thr Pro Thr Ser Pro Arg Arg
325 330 335

Tyr Ser Pro Val Ala Lys Asp Leu Leu Gly Glu Glu Asp Ile Pro Arg
340 345 350

Glu Pro Arg Arg Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly Phe
355 360 365

Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile
370 375 380

Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp
385 390 395 400

Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His Glu
405 410 415

Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile Ile
420 425 430

Ala Gln Tyr Lys Pro Glu Glu Tyr Ser Arg Phe Glu Ala Lys Ile His
435 440 445

Asp Leu Arg Glu Gln Leu Met Asn Ser Ser Leu Gly Ser Gly Thr Ala
450 455 460

Ser Leu Arg Ser Asn Pro Lys Arg Gly Phe Tyr Ile Arg Ala Leu Phe
465 470 475 480

Asp Tyr Asp Lys Thr Lys Asp Cys Gly Phe Leu Ser Gln Ala Leu Ser
485 490 495

Phe Arg Phe Gly Asp Val Leu His Val Ile Asp Ala Ser Asp Glu Glu
500 505 510

Trp Trp Gln Ala Arg Arg Val His Ser Asp Ser Glu Thr Asp Asp Ile
515 520 525

Gly Phe Ile Pro Ser Lys Arg Arg Val Glu Arg Arg Glu Trp Ser Arg
530 535 540

Leu Lys Ala Lys Asp Trp Gly Ser Ser Ser Gly Ser Gln Gly Arg Glu
545 550 555 560

Asp Ser Val Leu Ser Tyr Glu Thr Val Thr Gln Met Glu Val His Tyr
565 570 575

Ala Arg Pro Ile Ile Ile Leu Gly Pro Thr Lys Asp Arg Ala Asn Asp
580 585 590

Asp Leu Leu Ser Glu Phe Pro Asp Lys Phe Gly Ser Cys Val Pro His
595 600 605

Thr Thr Arg Pro Lys Arg Glu Tyr Glu Ile Asp Gly Arg Asp Tyr His
610 615 620

Phe Val Ser Ser Arg Glu Lys Met Glu Lys Asp Ile Gln Ala His Lys
625 630 635 640

Phe Ile Glu Ala Gly Gln Tyr Asn Ser His Leu Tyr Gly Thr Ser Val
645 650 655

Gln Ser Val Arg Glu Val Ala Glu Gln Gly Lys His Cys Ile Leu Asp
660 665 670

Val Ser Ala Asn Ala Val Arg Arg Leu Gln Ala Ala His Leu His Pro
675 680 685

Ile Ala Ile Phe Ile Arg Pro Arg Ser Leu Glu Asn Val Leu Glu Ile
690 695 700

Asn Lys Arg Ile Thr Glu Glu Gln Ala Arg Lys Ala Phe Asp Arg Ala
705 710 715 720

Thr Lys Leu Glu Gln Glu Phe Thr Glu Cys Phe Ser Ala Ile Val Glu
725 730 735

Gly Asp Ser Phe Glu Glu Ile Tyr His Lys Val Lys Arg Val Ile Glu
740 745 750

Asp Leu Ser Gly Pro Tyr Ile Trp Val Pro Ala Arg Glu Arg Leu
755 760 765

<210> 14
<211> 512
<212> PRT
<213> Homo sapiens

<400> 14

Met Glu Arg Ala Arg Lys Phe Ser Gly Ser Gly Leu Ala Met Gly Leu
1 5 10 15

Gly Ser Ala Ser Ala Ser Ala Trp Arg Arg Ala Ser Gln Arg Trp Ala
20 25 30

Trp Pro Leu Arg Ser Leu Arg Pro Gly Gly Asp Ala Arg Glu Pro Arg
35 40 45

Lys Ile Ile Leu His Lys Gly Ser Thr Gly Leu Gly Phe Asn Ile Val
50 55 60

Gly Gly Glu Asp Gly Glu Gly Ile Phe Val Ser Phe Ile Leu Ala Gly
65 70 75 80

Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Arg Gly Asp Arg Ile Leu
85 90 95

Ser Val Asn Gly Val Asn Leu Arg Asn Ala Thr His Glu Gln Ala Ala
100 105 110

Ala Ala Leu Lys Arg Ala Gly Gln Ser Val Thr Ile Val Ala Gln Tyr
115 120 125

Arg Pro Glu Glu Tyr Ser Arg Phe Glu Ser Lys Ile His Asp Leu Arg
130 135 140

Glu Gln Met Met Asn Ser Ser Met Ser Ser Gly Ser Gly Ser Leu Arg
145 150 155 160

Thr Ser Glu Lys Arg Ser Leu Tyr Val Arg Ala Leu Phe Asp Tyr Asp
165 170 175

Arg Thr Arg Asp Ser Cys Leu Pro Ser Gln Gly Leu Ser Phe Ser Tyr
180 185 190

Gly Asp Ile Leu His Val Ile Asn Ala Ser Asp Asp Glu Trp Trp Gln
195 200 205

Ala Arg Leu Val Thr Pro His Gly Glu Ser Glu Gln Ile Gly Val Ile

210 215 220

Pro Ser Lys Lys Arg Val Glu Lys Lys Glu Arg Ala Arg Leu Lys Thr
225 230 235 240

Val Lys Phe His Ala Arg Thr Gly Met Ile Glu Ser Asn Arg Ser Ile
245 250 255

Lys Thr Lys Arg Lys Lys Ser Phe Arg Leu Ser Arg Lys Phe Pro Phe
260 265 270

Tyr Lys Ser Lys Glu Asn Met Ala Gln Glu Ser Ser Ile Gln Glu Gln
275 280 285

Gly Val Thr Ser Asn Thr Ser Asp Ser Glu Ser Ser Ser Lys Gly Gln
290 295 300

Glu Asp Ala Ile Leu Ser Tyr Glu Pro Val Thr Arg Gln Glu Ile His
305 310 315 320

Tyr Ala Arg Pro Val Ile Ile Leu Gly Pro Met Lys Asp Arg Val Asn
325 330 335

Asp Asp Leu Ile Ser Glu Phe Pro His Lys Phe Gly Ser Cys Val Pro
340 345 350

His Thr Thr Arg Pro Arg Arg Asp Asn Glu Val Asp Gly Gln Asp Tyr
355 360 365

His Phe Val Val Ser Arg Glu Gln Met Glu Lys Asp Ile Gln Asp Asn
370 375 380

Lys Phe Ile Glu Ala Gly Gln Phe Asn Asp Asn Leu Tyr Gly Thr Ser
385 390 395 400

Ile Gln Ser Val Arg Ala Val Ala Glu Arg Gly Lys His Cys Ile Leu
405 410 415

Asp Val Ser Gly Asn Ala Ile Lys Arg Leu Gln Gln Ala Gln Leu Tyr
420 425 430

Pro Ile Ala Ile Phe Ile Lys Pro Lys Ser Ile Glu Ala Leu Met Glu
435 440 445

Met Asn Arg Arg Gln Thr Tyr Glu Gln Ala Asn Lys Ile Tyr Asp Lys
450 455 460

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Ala Met Lys Leu Glu Gln Glu Phe Gly Glu Tyr Phe Thr Ala Ile Val
465                 470                 475                 480

Gln Gly Asp Ser Leu Glu Glu Ile Tyr Asn Lys Ile Lys Gln Ile Ile
                485                 490                 495

Glu Asp Gln Ser Gly His Tyr Ile Trp Val Pro Ser Pro Glu Lys Leu
            500                 505                 510
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<210> 15
<211> 178
<212> PRT
<213> Homo sapiens

<400> 15

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Met Pro Lys Ala Lys Gly Lys Thr Arg Arg Gln Lys Phe Gly Tyr Ser
1               5                   10                  15

Val Asn Arg Lys Arg Leu Asn Arg Asn Ala Arg Arg Lys Ala Ala Arg
            20                  25                  30

Gly Ile Glu Cys Ser His Ile Arg His Ala Trp Asp His Ala Lys Ser
        35                  40                  45

Val Arg Gln Asn Leu Ala Glu Met Gly Leu Ala Val Asp Pro Asn Arg
    50                  55                  60

Ala Val Pro Leu Arg Lys Arg Lys Val Lys Ala Met Glu Val Asp Ile
65                  70                  75                  80

Glu Glu Arg Pro Lys Glu Leu Val Arg Lys Pro Tyr Val Leu Asn Asp
                85                  90                  95

Leu Glu Ala Glu Ala Ser Leu Pro Glu Lys Lys Gly Asn Thr Leu Ser
            100                 105                 110

Arg Asp Leu Ile Asp Tyr Val Arg Tyr Met Val Glu Asn His Gly Glu
        115                 120                 125

Asp Tyr Lys Ala Met Ala Arg Asp Glu Lys Asn Tyr Tyr Gln Asp Thr
    130                 135                 140

Pro Lys Gln Ile Arg Ser Lys Ile Asn Val Tyr Lys Arg Phe Tyr Pro
145                 150                 155                 160

Ala Glu Trp Gln Asp Phe Leu Asp Ser Leu Gln Lys Arg Lys Met Glu
                165                 170                 175
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Val Glu

<210> 16
<211> 221
<212> PRT
<213> Homo sapiens

<400> 16

Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
1 5 10 15

Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
20 25 30

Met Arg Met Thr Arg Ser Val Asp Asn Val Arg Phe Leu Pro Phe Leu
35 40 45

Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
50 55 60

Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
65 70 75 80

Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
85 90 95

Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
100 105 110

Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
115 120 125

Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
130 135 140

Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
145 150 155 160

Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
165 170 175

Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
180 185 190

Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr

195 200 205

Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
210 215 220